

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:44:38 ; Search time 44 Seconds
(without alignments)
1626.938 Million cell updates/sec

Title: US-10-782-570-2
Perfect score: 3906
Sequence: 1 MNQNNNEYIIDSKNLSYP.....PFTNHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	29.7	1180	2 A26858	parasporal crystal
2	1158	29.6	1180	2 I39870	parasporal crystal
3	923.5	23.6	934	2 B29838	parasporal crystal
4	819	21.0	1136	1 US8581	parasporal crystal
5	710	18.2	659	2 S10228	parasporal crystal
6	695	17.8	652	2 I39811	parasporal crystal
7	692	17.7	1138	2 A48944	parasporal crystal
8	676	17.3	1160	2 I40589	parasporal crystal
9	659.5	16.9	1157	1 S49247	parasporal crystal
10	620.5	15.9	652	2 A27323	parasporal crystal
11	611	15.6	1228	2 S00873	parasporal crystal
12	588.5	15.1	719	2 I39815	insecticidal prote
13	585.5	15.0	719	2 I39814	insecticidal prote
14	585.5	15.0	719	2 S25383	parasporal crystal
15	578	14.8	649	1 JH0261	parasporal crystal
16	576	14.7	1165	2 S11446	parasporal crystal
17	573	14.7	1178	1 USBSXH	parasporal crystal
18	563.5	14.4	719	2 I40590	crv465 protein -
19	563.5	14.3	1177	2 A49785	parasporal crystal
20	551	14.1	1154	2 S39536	parasporal crystal
21	540.5	13.8	1171	2 A37829	parasporal crystal
22	540.5	13.8	1171	2 I40572	parasporal crystal
23	538	13.8	1176	2 S32649	parasporal crystal
24	534.5	13.7	1176	2 A48970	parasporal crystal
25	528	13.5	618	2 S11445	parasporal crystal
26	526.5	13.5	655	2 JCT140	protoxin - Bacillu
27	522.5	13.4	823	2 S04181	parasporal crystal
28	519.5	13.3	1174	2 A42459	parasporal crystal
29	517.5	13.2	1160	2 S32647	parasporal crystal

RESULT 1

A26858

Parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis
N;Alternate names: parasporal crystal protein cryIVA
C;Species: Bacillus thuringiensis subsp. israelensis
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004
C;Accession: A26858; S48691
R;Ward, E.S.; Ellar, D.J.

Nucleic Acids Res. 15, 7195, 1987

A;Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding
A;Reference number: A26858; MUID:88015571; PMID:2821500
A;Accession: A26858

A;Molecule type: DNA

A;Residues: 1-1180 <VAR>

A;Cross-references: UNIPROT:P16480; UNIPARC:UPI000016EA42; GB:Y00423; NID:940351; PIDN:C

A;Note: the authors translated the codon GCA for residue 308 as Thr

R;Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.

FEBS Lett. 348, 249-254, 1994

A;Title: Functional analysis of block 5, one of the highly conserved amino acid sequence

A;Reference number: S48691; MUID:94307434; PMID:7913448

A;Accession: S48691

A;Molecule type: DNA

A;Residues: 667-676 <NIS>

A;Cross-references: UNIPARC:UPI000017819A

C;Superfamily: Parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 29.7%; Score 1159; DB 2; Length 1180;
Best Local Similarity 37.3%; Pred. No. 1.2e-64;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy	5	NNNEYEII	DS--KNLSYPSNRNIDHSYVPTNNPNQPLQNTNYKEWLNMCQNTQYGDNF	62
Db	6	NKNSEYTNASQK	KLINSN-----YTRYPIENSFKQLQSTNYKDWLNMCQNTQYGDNF	61
Qy	63	ETFSADPTIAA	VSAGTIVSGTLLAGIGLTSISGPIGIIAIIISFGTLITVFPAGBQD	122
Db	62	ETFDIDS---	GELSAVTIVGVTLTGFGTT----PLGL---ALIGFGTLIPVLPFAQDQS	111
Qy	123	KTVMTQIKGEI	FVDFPTLPTESIKQLKQTLLEGFRQLQSNTALDDWRKUKRLQAPGLP	182
Db	112	NT-MSDFITQT	KNIKKKEIASTYISNANKILNRSFNVIISTYHNHLKTWE-----NNPNPQ	165
Qy	183	PSSALQQAALT	KLTRFENVHNDFFIREIP--GFQLETYKTLTLLPIYAQAANFHLNLLQQA	240
Db	166	NTQDVRTQIQ	LVHVFQNVIPDELVNSCPNPSDDCYNINLVSSYAQAANLHLLTVINQAV	225
Qy	241	ELADEWNAD	IHPSOIEPNAGTSDDDYKLLKENIKPYSNYCANTYREGLNKLNRNEP-----	295
Db	226	KFEAYLKNRQ	FDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLIKTTTPDSNLD	284
Qy	296	-NMRWSIFND	YRRYWTITVLDITIAQFSFYDIKRYKDSIGRIGGIKTELTRTIYTYTEINF	354

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Db 285 GNINMNTYNTYRTKMTTAVLDVVALPNYDVGKYP-----GVQSELTRIIYQV-LNPE 337
QY 355 RLTYLEIOPNLAMEYNLTRSGRLRFSFLDELFTYKNETYGNRLVGIANRSTYA--- 411
Db 338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSLNFYEKAQOTTPNFF--TSHYNNMFHYTLDN 393
QY 412 TTGTETIYIGERTGPTTKTLIPESYKVSIVTDQVTPSPPNIVFTINOIELYLNNSP 471
Db 394 ISOKSVFGHNVTDKLSL--GLATNIYIFLNLVSLDNKYLDNYYNISKMDFFITNGT 451
QY 472 ---SNKLTYSAGGNSDKKTTDFQFPVKDCPKPIPNPNCPLSYNSYSHILSOFSLFNY- 527
Db 452 RLLEKELT-AGSGQITVDVKNKIFGLPIKRRNQGNPTLFTPYDNYSHILSFIKLSIP 510
QY 528 -SYKIGLALNILYTGALGWTSHSSVNRNNAISDKIITMIPAKNSLDTSNKSVEGPGHTG 586
Db 511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVVGPGHTG 563
QY 587 GNLVYLQSGRLEITCRTPNSTOSYIRLRYATNGAGNTLPNLSLTIPGVIGIPPQRLNN 646
Db 564 GDLI--DFKDHFKITCQHSNFQOSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
QY 647 TFSGTNNNLQYDGFQFPFSTVTLPLNRNIPFIFNRADV-SNSILIIDKIEFIPITS 705
Db 621 TFSGTDYTNLYKDFQYLEFSNEVPAPQNISLVFNRSVDYNTVTLIDKIEFLPITS 680
QY 706 VRQNRKQKLETTQTKINTFTNHTKNTLNIBATNYDID 744
Db 681 IREDREKQKLETVQOIINTFYANPIKNTLQSELTDYDID 719

RESULT 2
I39870
parasporal crystal protein ISRH4 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
R:Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,
Agric. Biol. Chem. 52, 873-878, 1988
A>Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes
A:Reference number: I39869
A:Accession: I39870
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1180 <RES>
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI0000001B1F; GB:D00248; NID:g216289; PIDN:
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 29.6%; Score 1158; DB 2; Length 1180;
Best Local Similarity 37.3%; Pred. No. 1.3e-64;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

QY 5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNPNQPLQNTNYKEWLMCMQGNTOYGDNF 62
Db 6 NKNEYETLASQKKLAINSN---YTRYPIENSPKQLLQSTNYKDWLMCMQCNQYGGDF 61

QY 63 ETFSADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAILIISFGTLITVFWPAGEQD 122
Db 62 ETFTDS---GELSAITVVGTLVTFGFTT---PLGL---ALIGFTGLIPVLFPAQDQS 111

QY 123 KTWTFQIKMGEIFVDTPLTESIKQLQTLLEGFRILQSYNTALDDWRKLRQLRGLP 182
Db 112 NT-WSDFITQTKNIIEKKEIASTYISNANKTLNRSFNVIYTHNLKLTWE-----NNPNPQ 165

QY 183 PSSALQQAALTLRKRFENVHDFIREP--GFOLEYTKTLPIYAAQANFHLNLQOGA 240
Db 166 NTQDVRTQIQLVHVFQNVLPVNSCPNPSDCDYNNILVLSYAAQANLHLTVLNQAV 225

QY 241 ELADEWNADITHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP----- 295
Db 226 KPEAYLKNNRQFOYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLIKTTTPDSNLD 284
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QY 296 -NWRMSIFNDYRYMTITVLDLIAQSFYDIKRYKDSIGRIGIKTELTRIIYTTAINED 354
Db 285 GNINMNTYNTYRTKMTTAVLDVVALPNYDVGKYP-----GVQSELTRIIYQV-LNPE 337
QY 355 RLTYLEIOPNLAMEYNLTRSGRLRFSFLDELIFTKNETYGNRLVGIANRSTYA--- 411
Db 338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSLNFYEKAQOTTPNFF--TSHYNNMFHYTLDN 393
QY 412 TTGTETIYIGERTGPTTKTLIPESYKVSIVTDQVTPSPPNIVFTINOIELYLNNSP 471
Db 394 ISOKSVFGHNVTDKLSL--GLATNIYIFLNLVSLDNKYLDNYYNISKMDFFITNGT 451
QY 472 ---SNKLTYSAGGNSDKKTTDFQFPVKDCPKPIPNPNCPLSYNSYSHILSOFSLFNY- 527
Db 452 RLLEKELT-AGSGQITVDVKNKIFGLPIKRRNQGNPTLFTPYDNYSHILSFIKLSIP 510
QY 528 -SYKIGLALNILYTGALGWTSHSSVNRNNAISDKIITMIPAKNSLDTSNKSVEGPGHTG 586
Db 511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVVGPGHTG 563
QY 587 GNLVYLQSGRLEITCRTPNSTOSYIRLRYATNGAGNTLPNLSLTIPGVIGIPPQRLNN 646
Db 564 GDLI--DFKDHFKITCQHSNFQOSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
QY 647 TFSGTNNNLQYDGFQFPFSTVTLPLNRNIPFIFNRADV-SNSILIIDKIEFIPITS 705
Db 621 TFSGTDYTNLYKDFQYLEFSNEVPAPQNISLVFNRSVDYNTVTLIDKIEFLPITS 680
QY 706 VRQNRKQKLETTQTKINTFTNHTKNTLNIBATNYDID 744
Db 681 IREDREKQKLETVQOIINTFYANPIKNTLQSELTDYDID 719

RESULT 3
B29838
parasporal crystal protein - Bacillus thuringiensis subsp. israelensis (fragment)
C:Species: Bacillus thuringiensis subsp. israelensis
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: B29838
R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.
J. Bacteriol. 166, 801-811, 1986
A>Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
A:Reference number: A94672; MUID:86223796; PMID:3011746
A:Accession: B29838
A:Molecule type: DNA
A:Residues: 1-934 <THO>
A:Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g143228

Query Match 23.6%; Score 923.5; DB 2; Length 934;
Best Local Similarity 32.7%; Pred. No. 5.1e-50;
Matches 262; Conservative 117; Mismatches 270; Indels 153; Gaps 34;

QY 5 NNNEYEIDSKNLSYPSNRNIDHSRYPTNPNQPLQNTNYKEWLMCMQGNTOYGDNFET 64
Db 6 NKNEYEIFNAPNGSGSKSN--YSRYPLANKENQPLKNTNYKDWLVNVCQDNQYGNAGN 63

QY 65 ETFSADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAILIISFGTLITVFWPAGEQDKT 124
Db 64 FASSETIVGVSAGIIVGVTMLG-----AFAAP--VLAAGIISFGTLIPFW-QGSDPAN 114

QY 125 VNTQTFIKMGEIFVDTPLTB---SIKQLKLTLEGFRILQSYNTALDDWRKLRQLRQAPGL 181
Db 115 VMQDLNIG---GRPIQIDKNINVLTSIVTPKNQLDKQEFDFKKWEPAR----- 163

QY 182 PPSALQQAALTLRKRFENVH--DFIREIFGQLEYTKTLPIYAAQANFHLNLQO 238
Db 164 --THANAKAVHDLFTTLEPIIDKLDMLKNNASYRIPT-----LPAYAQIATWHLNLLKH 216

QY 239 GAELEADWNADITHPQIEPNAGTSDDYK-LKENIPKYSNYCANTYRGLNKLNEP 297
Db 217 AATYTNIW---LQNOGINPSTFNSSNYQYGLRKRKIQBYTDYCIQTYNAGLTWIRTNTNA 273
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Db 575 PNNIPTDLKYEFYKDPDAIPVPMELSSQLITIAIQPLNMTSNNOVIIDRIEIPIT 634
Qy 704 SSYRONREKQKLTIOKINTFTNTHTKNTLNIETATNYDID 744
Db 635 QSVLDETENQNLSEREVNALFTNDKADALNIGTIDYDID 675
RESULT 5
S10228
Parasporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
N;Alternate names: coleopter-an active parasporal crystal protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S10228
R;Sick, A.; Gaertner, F.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A;Title: Nucleotide sequence of a coleopter-an active toxin gene from a new isolate of Ba
A;Reference number: S10228; MUID:90206811; PMID:2320431
A;Accession: S10228
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-659 <SIC>
A;Cross-references: UNIPROT:P17969; UNIPARC:UPI0000126C13; EMBL:X17123; NID:g40258; PIDN:
C;Genetics:
A;Gene: cryIIIB
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin; toxin
Query Match 18.2%; Score 710; DB 2; Length 659;
Best Local Similarity 28.9%; Pred. No. 7.9e-37;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;
Qy 1 MNQNNNEYIID-SKNLSPSNRNIHDSRYPTNNPQNPQNTNYKEWLNMCQNTQYG 59
Db 9 MNPNNRSEYDTIKVTPNSELPNTN-----HNQYPLADNPNTLEELNYKEFLRMTADNST-- 62
Qy 60 DNPETASADTTAAVSGAGTIVSGTLGAGIGLTSISGPIIGIIGAIISFGTLITVFWPAG 119
Db 63 ---EVLDSSTVKDVGTVGIVSVQILGVVG-----VPPAGALTSTFYQSFLNALWPS- 110
Qy 120 EQDKTVMTQIKMGEIFVDTPLTESIKQLKQLTLEGFRQILQSYNTALDDWRKLRLOAP 179
Db 111 --DADPWKAFMAQVEVLIDKKIBEYAKSKALAEQLQNNFEDYVNALDSWKK----- 161
Qy 180 GLPSSALQQAALTALKIRFENVHDFIREIPGFQLETYKTLPIYAQAANFHLNLQOG 239
Db 162 -APVNLRSQRDIRELFSQAESHFRNSMPSFAVSKFVLFLPTYAQAANTHLLLLKOA 220
Qy 240 AELADEWNADIHPSQIEPNAGTSD--YVKLKENIPKYSNCANTYREGLNKLRNEPN 296
Db 221 QVFGEEWY-----SSEDIAEFYQKQLTQYTDHCVNWNVGNLSRGSTY 268
Qy 297 MRWSIENDYRYMTITVLDTIAQSFYDIKRYKDSIGRIGIKTELTRIETITTEINPDL 356
Db 269 DAWVKFNRRFRETTLVLDLIVLFPFYDRLYSK-----GVKTELTRDITDPI-FTLN 321
Qy 357 TYLEIOPNLAIMENYLRSGRLFSFLDELIFYTK-----NETYGNRLVGIANR 405
Db 322 ALQYGTFTFSIENSIRKP--HLFDYLRGIEFTRLRPGYSGKDSFNWWSGNY---VETR 376
Qy 406 NRSTYATGTETIYGERGTGPTTKTLIPESYKSVIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSFDGQKVY----RTIANTDIAAFPDKIYFGVT 430
Qy 462 QIBLYLNNSPSKNL---TYSA-----GGLNSDK---KTTFDQFPVKCKPCKPIINPNC 508
Db 431 KVDPSQYDDQKNETSTQTYDSKRYNGYLGQAQSDIDQLPPETTD--BPLEK----- 478
Qy 509 LPSYNSYSHITLSQSFNYSYKIGLALNILYTGALGTHSSVNRNNAISDKIITMIPAK 568
Db 479 -----AYSHQNLNAECLMQDRGTI--PPFT-----WTHRSVDFFNTIDAEKITQLPVVK 527
Qy 569 GNSLDTNSKVIIEGFGHTGGNLVYLQ-----SQGRLEITCRTPNSTQSYIYRLRYATNGAGN 624

Db 528 AYALSSGASIIIEGPGFTGCGNLLFLKSSNSIAKPKVTLNSAALLQRYRYRIRVAST---- 583
Qy 625 TLPNLSLTTPGVIGIPPPQRLNNTFSGTNVNNLOY--GDFGY--FQPPSTVTUPLNRNIPP 680
Db 584 --TNLRLFV-----QNSNDFLVIYINKMTNIDGDLTYQTFDPATS-----NSNMGF 628
Qy 681 IFNRAD-----VSNLSILIIDKIEFPI 702
Db 629 SGGTNDFTIGABSFVSNKIIYIDKIEFIPV 658
RESULT 6
I39811
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIB2
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C;Accession: I39811
R;Donovan, W.P.; Rupan, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.B.
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys
A;Reference number: I39811; MUID:93119147; PMID:1476436
A;Accession: I39811
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-652 <RES>
A;Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:
C;Genetics:
A;Gene: cryIIIB2
C;Superfamily: Parasporal crystal protein
Query Match 17.8%; Score 695; DB 2; Length 652;
Best Local Similarity 28.4%; Pred. No. 6.8e-36;
Matches 209; Conservative 121; Mismatches 286; Indels 120; Gaps 28;
Qy 1 MNQNNNEYIIDSKNLSPSNRNIHDSRYPTNNPQNPQNTNYKEWLNMCQ-GNTQYG 59
Db 1 MNPNNRSEHDTI---KVTNSELTQNHQYPLADNPNTLEELNYKEFLRMTDSSTVL 57
Qy 60 DNPETASADTTA-AVSGATIVSGTLGAGIGLTSISGPIIGIIGAIISFGTLITVFWPA 118
Db 58 DN-----STVKDVGTVGIVSVQILGVVG-----VPPAGALTSTFYQSFLANTWPS 102
Qy 119 GQDKTVMTQIKMGEIFVDTPLTESIKQLKQLTLEGFRQILQSYNTALDDWRKLRLOA 178
Db 103 ---DADPWKAFMAQVEVLIDKKIBEYAKSKALAEQLQNNFEDYVNALSWKK----- 153
Qy 179 PGLPSSALQQAALTALKIRFENVHDFIREIPGFQLETYKTLPIYAQAANFHLNLQO 238
Db 154 --TPLSLRSQRDIRELFSQAESHFRNSMPSFAVSKFVLFLPTYAQAANTHLLLLKD 211
Qy 239 GAELADEWNADIHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGLNKLRNEPNR 298
Db 212 AQVFGEEWYS-----SEDAVFYRQLKLT-QQYTDHCVNWNVGNLSRGSTYDA 262
Qy 299 WSIENDYRYMTITVLDTIAQSFYDIKRYKDSIGRIGIKTELTRIETITTEINPDLTY 358
Db 263 WVKFNRRFRETTLVLDLIVLFPFYDRLYSK-----GVKTELTRDITDPI-FTLN 315
Qy 359 LBIQNLAIMENYLRSGRLFSFLDELIFYTK-----NETYGNRLVGIANRR 407
Db 316 QYVGTFTFSIENSIRKP--HLFDYLRGIEFTRLRPGYSGKDSFNWWSGNY---VETRPS 370
Qy 408 STYATGTETIYGERGTGPTTKTLIPESYKSVIVTDQV--TPTSPPN--IYFTINQI 463
Db 371 IGSSKTTITSPFYGDKSTEVQK--LSFDGQKVY----RTIANTDIAAAMPNGKVLGVTKV 424
Qy 464 ELYLNNSPSKNL---TYSA---GGLNSDKKTTDQFPVKCKPCKPIINPCLPSYNSYSH 517
Db 425 DPSQYDDQKNETSTQTYDSKRYNGYVSAQSDID--QLPPTTDEPL-----EKAYSH 474
Qy 518 ILSQSFLEFNYSYKIGLALNILYTGALGTHSSVNRNNAISDKIITMIPAKGNSLDTNSK 577

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Db 475 QLNVAECFLMODRGTI--PFET-----WTHRSVDFFNTIDAETQLQFPVKAYALSSGAS 528
Qy 578 VIEGPGHTGGLVYLQ-----SOGLEITCRPNSTQSYIRLRVATNGAGNTLPLNISLTI 633
Db 529 IIEGPGTGGNLLFLKESNSIAFKVTLNSAALLQRYVRIRVAST-----TNRLFLV 582
Qy 634 PGVIGIPQRLNNTFTGNYN-----NLQYGFQYFPQPPSTVTLPLNRNIPPIFNAD 686
Db 583 -----QNSNDFLVYINKTNKDDLLTYQTFDLATTNSNMFGSDKNELIIGAESF 634
Qy 687 VNSILAIIDKIEFTPI 702
Db 635 VSNEKIYIDKIEFIPV 650

RESULT 7
A48944
Parasporal crystal protein cry7Aa1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIC
C;Species: Bacillus thuringiensis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A48944
R;Lambert, B.; Hofte, H.; Anyas, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit
A;Reference number: A48944; MUID:92384571; PMID:1514800
A;Contents: BVS137J
A;Accession: A48944
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-1138 <LAM>
A;Cross-references: UNIPROT:Q03749; UNIPARC:UPI000002C1E6; GB:M64478; NID:G142760; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 17.7%; Score 692; DB 2; Length 1138;
Best Local Similarity 28.3%; Pred. No. 2.4e-35;
Matches 221; Conservative 127; Mismatches 288; Indels 146; Gaps 33;
Qy 1 MNQNNNEYIIDSKNLSYPSNRNIDHS-RYPYNNPNQPLONTNYKSWLNMCOGNTQYG 59
Db 1 MNLNLDGYE-----DSNRTLNLSNLYPTQKALSPSLKNNYQDFLSITE-----R 46
Qy 60 DNPETPASADTIAAVSAGTIIVSGTLLAGIGLTSISGPIGIGAIITS--FGTLITVFWP 117
Db 47 EQPALLASGNT--AINTVSVIGATLSA-----LGVPGASFITNFYKTAGLWMP 94
Qy 118 AGEQDKTWVTFQIKWGEIFVDTPLETESIKQLKLTLEGFRQILQSYNTALDDWRKLRQL 177
Db 95 --ENKGIWDFMTEVEALIDQKIEEYVRNKAIAELDGLGSALDKYQKALADW--LGKQD 149
Qy 178 APGLPPSALQQAALTUKIRFENVHNDPIREIPGQLEYTKLLPLPIYAQAANFHLNLLQ 237
Db 150 DP-----EAILSTAFERIIDSLFEFSMPFKVTGYEIPILLTYVAQAANLHALLR 200
Qy 238 QGAELADENADIHPSOLEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNKLNRPNM 297
Db 201 DSTLYGKWG--FTQNNIEN-----YNRQKRISYSDHCYKTNVNSGLRSLNGSYE 251
Qy 298 RWSIFNDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIGKTELREIYITTEINFDRLT 357
Db 252 QWINYNFRREMILMALDVLAVFPFHPDRRYSME-----TSTQLTREYVTDVPSLS-IS 304
Qy 358 YLEIQPNLAIMEYNLTRSGLRFLSFLDELIPYT-KNETYGNRL-----VGIANR 405
Db 305 NPDIGSPFSQMENTAIRTP-HLVYLDDELITYTSKYKAFSHEIQPDLFYNSAHKVSFKKS 363
Qy 406 NRSTVATTGTETIYXGRTGPPTTKTLIPFESYKYSIVTDQVTPSTSPNNIY-----FTI 460
Db 364 EQSNLYTTG---YKGTSG-----YISSGAYSFH-GNDIYRTLAAPSVVVPYPTQYGV 413
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Qy 461 NQIELY-----LNNSPENK--LTVSAGGNLSNDKTTDFQFPVKKOCKPIINPNCLPSYN 513
Db 414 EQVEFYGVKGVHVRGDNKYDLTYDSIDQLPPDGE-----PIHE 452
Qy 514 SYSHILSQ-PSEFNYSYKIGLALNLTGALGWTHTSSVNRNNAISDKLITMIPAIGNSL 572
Db 453 KYTHRLCHATAIFKSTPDYDNATIPFS-----WTHRSAEYNNRIYPNKITKIPAVOMYKL 508
Qy 573 DTNSKVIEGPGHTGGLNLYVLQSQGRLEITCRTPNS--TQSYIRLRVATNGAG--NTLPLN 628
Db 509 DDPSTVVKGPGFTGGDLVKEGSTYIGDIKATVNSPLSQKYRVRVATNVSSGQFNYYIN 568
Qy 629 ISLTIPGVIGIPQRLNNTFTSGT-----NWNLYQGFQYFPQPPSTVTLPLNRNIPPIFN 683
Db 569 DKIT-----LQTKFQNTVETIGEGKDLTYGSFGYIEYSTTIQFP-DEHPKITLH 616
Qy 684 RADVS-NSILLIDKIEPIPTSSVRQNRREKQLETIQTKINTPTNTKNTLNTLEATNYD 742
Db 617 LSDLSNNSPFYDSIEFIPVDVNY---AEKEKEKAQKAVNTLFT-BGRNALQKQVTDYK 672
Qy 743 ID 744
Db 673 VD 674

RESULT 8
I40589
Parasporal crystal protein cry8Ca1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIII
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C;Accession: I40589
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curt. Microbiol. 28, 15-19, 1994
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Reference number: I40589; MUID:94100786; PMID:7764305
A;Accession: I40589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1160 <RES>
A;Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CFE; EMBL:U04366; NID:G532523; PID
C;Superfamily: Parasporal crystal protein
C;Keywords: Delta-endotoxin

Query Match 17.3%; Score 676; DB 2; Length 1160;
Best Local Similarity 27.7%; Pred. No. 2.5e-34;
Matches 217; Conservative 122; Mismatches 317; Indels 128; Gaps 29;
Qy 1 MNQNNNEYIIDSKNLSYPSNRNIDHSRYPYNNPNQPLONTNYKSWLNMCOG-NTQYG 59
Db 1 MSPNNQNEYIIDSALSPTSVSDNSI---RYPLANDQNTLTQNNMYKDYLKMTSTNAELS 57
Qy 60 DNPETPASADTIAAVSAGTIIVSGTLLAGIGLTSISGPIGIGAIITSFGTLITVFWPAG 119
Db 58 RNPGTFTISAQ--AVGTGDIVSTIISGLG-----IPVLGEVFSILGSLGLWPSN 107
Qy 120 EQDKTWVTFQIKWGEIFVDTPLETESIKQLKLTLEGFRQILQSYNTALDDWRKLRQAP 179
Db 108 NEN--VWQIFPNRVEELIDQKILDSVRSRAIDLANSRIAVEYYQNALEDWRK----- 158
Qy 180 GLPPSSALQQAALTUKIRFENVHNDPIREIPGQLEYTKLLPLPIYAQAANFHLNLLQ 239
Db 159 --NPHST--RSAALVKERFGNAAILRTNMGSFQNTNYETPLPLTYAQAASLHLLVMRDV 214
Qy 240 AELADENADIHPSOLEPNAGTSDDYKLLKENIPKYSNYCANTYREGLNKLNRPNMRW 299
Db 215 QIYKKEWG---YPO-----NDIDLIFYKEQVSRYTARYSDHCYQVYNAGLNKLRGTGAKQW 265
Qy 300 SIFNDYRRYMTITVLDITIAQFSFYDIKRYKDSIGRIGGIGKTELREIYITTEINFDRLT 357
Db 266 VDYNRFRREMVMVLDVLAVFPYD-----ARIYPLETNAELTETFTDPVG-----S 313
Qy 358 YLEIQPNLAIMEYNLTRSGLRFLSFLDELI-----FYTKNETYGNRLVGIANRNRSTVATT 413
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Db 314 YVTGQSSTLISWYDMIPAAALPSPSTLENLLRKDPDFTLLQEI-----RWYTSFRQW 364
Qy 414 GTIILIGERTGPTTKTLI---PPESYKVISVTDQVTPSTP-----FPNIY 457
Db 365 GTIEYNYMGQBLTLISYIGSSFNFKYSGLVLAGAEDIIPVGQNDIYRVVMWYIGRYTNSL 424
Qy 458 FTINOIELYLNNSPKNLTYSAGGNLSNDKKTDTDFQPVKKOCKPIINPNCLPSYNSYSH 517
Db 425 LGVNPVTFPSN--NTQKIYSKPKQAGGKTKTDSGEELTYE-----NYQSYSH 471
Qy 518 ILSQFSLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGKNSLDTNSK 577
Db 472 RVSYITSFEIKSTGGTVLGWV--PIFGWTHSSASRNFIYATKISQIPINKASR--TSGG 527
Qy 578 VI-----EGPQHTGCLNVLQSQ-----RLEITCRTPNSQSYIIRLYATNGAGN-TLPN 628
Db 528 AVNMFQGL--YNGGPNVKLSGSGSQVINLRVATDAKASQRYRIRIYASDRAGKFTISS 586
Qy 629 ISLTIPGVIGIPQRLN--NTEFGTNYNNLQYDGFYQFPSTVTVLPLNRNIPFIENRAD 686
Db 587 RSPENATYSASTAYNTWSTNASLTYSTPAYAESG-----PINLIGSGSRTED 636
Qy 687 VS-----NSILIDKIEFIPITPSVRQNRKOKLETIQTKINTFTNHTKNTLNIEATN 740
Db 637 ISITKEAGAAANLYIDRIEFIPVNTLF---EAEBDLVAKKAVNGLFTNE-KDALQTSVTD 692
Qy 741 YDID 744
Db 693 YQVN 696
RESULT 9
S49247
parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N;Alternate names: Parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C;Accession: A59350; S49247
R;Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai
A;Reference number: A59350; MUID:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residues: 1-1157 <LMS>
A;Cross-references: UNIPROT:Q45733; UNIPARC:UPI000002F5A5; EMBL:Z37527; NID:9547554; PID
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects,
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin
Query Match 16.9%; Score 659.5; DB 1; Length 1157;
Best Local Similarity 27.1%; Pred. No. 2.7e-33;
Matches 218; Conservative 118; Mismatches 298; Indels 171; Gaps 33;
Qy 1 MNQNNNEVEIIDSKNLSYPSNENIDHSRVPYTNPNQPLQNTYKELNWCQGNQYQGD 60
Db 1 MNRNNQNEVEIIDAPHCQPSD---DDVRYPLASDPAALQNNYKDYQMT--DEDTYD 55
Qy 61 NF-ETPASADTIAAVSAGTIVSGTLGAGIGGLTSGIPGIIIGALIIISFGTLITVFWPAG 119
Db 56 SYINPSLISIGRDAVQTALTVCVRLGALG-----VPFSQIYVSFYQFLLNTLWPV- 106
Qy 120 EQDKTWTQIKMGEIFVDTPLTESIKQLKQLTLEGFROILOSINTALDDW-----RK 172
Db 107 -NDTAIWEAFMRQVEELVNQOITEFARNQALARLOGLGDSFNYYQSRQNLWLADNRDTRN 165
Qy 173 LKELQAPGLPPSSALQQAALTAKIRENVHNDPIREIPGQLETYKTLTLLPIYAQAANFH 232
Db 166 LSVVRA-----QFIADL-----DFVNAIPLFVANGQQVPLLSVTAQAVNLH 207
Qy 233 LNLLOQGAELADEWNADIHPSQIEPNAGTSDDDYYKLLKENIPKYSNYCANTYREGLNKL 292

Db 208 LLLLDKASLFGSGWGF-----TQGEISTYDRQLELTAKYTNYCETWYNTGLDLRL 258
Qy 293 NEPNRWISLNDYRRYMYITVLDTIAQSFYDIKRYKDSIGRIGGKTKLTHRIIYTEIN 352
Db 259 GTNTESWLRVYHQFRREMTLVLDVVALFPYIVDRLYPT-----GSNPQLTREVVDPV 312
Qy 353 FD-----RLTYLEIQ-----PNLAIMEYNLTRSGRL-----PSFLDELIF 388
Db 313 FNPPANVGLCRWGTNPYNTFSELENAFIRPHLFDRLNSLTISSNRFVSSNFMWYWSG 372
Qy 389 YTKNETYGNRLV-----GIANRNRSTY--ATTGTEIIYGERTGPTTKTLIPFESYKVS 440
Db 373 HTLRSYLNDSAVQEDSYGLITTTTRATINPGVDGTRNI-----ESTAVDFRSALIG 423
Qy 441 IVTDKQVTPSPFPNIYFTINOIELYLNNSPKNLTYSAGGNLSNDKKTDTDFQPVKKDC 500
Db 424 IY-----GYNRASFPVGGFLFNG---TTS---PANGGC 449
Qy 501 KPIINPNC-LP---SYNSYSHILSQFSLFNYSYKIGLALNLYTGALG---WTHSSVNRN 553
Db 450 RDLVYNDDELPPDESTGSTRHLSHVTFP--SFQTNQAGSIANAGSVPTVWTRRDVDLN 507
Qy 554 NAISDKIITMIPAIGKNSLDTNSKVIIEGPGHTGGNLVYLSQ---GRLEITCRTPNSTQS 610
Db 508 NTITPNRITQLPLVKASAPVSGTTLVKGFGFTGGILRRRTTNGTFTGLRVTVNSP-LTQQ 566
Qy 611 YYIRLYATNGAGNTLPNISL-TIPGVIGIPQRLNNTFTSGTNYNNLQYDGFYQFPST 669
Db 567 YRLRVFASGT-----NFSIRVLRGGVSGIDVRLGSTMN--RGOELTYESFTTREF--T 616
Qy 670 VTPLNRNIPFIENRADVNSNI-----LIIDKIEFIPITPSVRQNRKOKLETIQ 719
Db 617 TTGPNP--PFTTQOEILTVNAGSVTGGYYIDRIEIVPNPA---REAEEDLEAAK 671
Qy 720 TKINTFFTNHTKNTLNIEATNYDID 744
Db 672 KAVASLFT-RTRDGLQVNVTDYQVD 695
RESULT 10
A27323
parasporal crystal protein cry3Aa1 - Bacillus thuringiensis
N;Alternate names: Coleopteran-specific insect control protein; crystal protein cryC; del
C;Species: Bacillus thuringiensis
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004
C;Accession: A27323; A26853; A29987; A28407; S60781; I39813
R;Herrnstadt, C.; Gilroy, T.E.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.
Gene 57, 37-46, 1987
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active del
A;Reference number: A27323; MUID:88112860; PMID:2828180
A;Accession: A27323
A;Molecule type: DNA
A;Residues: 1-652 <HER>
A;Cross-references: UNIPROT:Q9S6N9; UNIPARC:UPI00000AEBDC; GB:M22472; NID:gl42733; PIDN:f
A;Experimental source: strain San Diego
R;Hoefte H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.
Nucleic Acids Res. 15, 7193, 1987
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuri
A;Reference number: A26853; MUID:88015559; PMID:3658680
A;Accession: A26853
A;Molecule type: DNA
A;Residues: 9-652 <HOE>
A;Cross-references: UNIPARC:UPI000002B8CD; GB:Y00420; NID:g40252; PIDN:CAA68482.1; PID:g4
A;Experimental source: var. tenebrionis
R;McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.f
Bio/Technology 6, 61-66, 1988
A;Title: Characterization of the coleopteran-specific protein gene of Bacillus thuringier
A;Reference number: A29987
A;Accession: A29987
A;Molecule type: DNA
A;Residues: 9-652 <MCP>
A;Cross-references: UNIPARC:UPI000002B8CD

A;Experimental source: var. tenebrionis
R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987
A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene
A;Reference number: A28407
A;Accession: A28407
A;Molecule type: DNA
A;Residues: 9-652 <SEK>
A;Cross-references: UNIPARC:UPI000002B8CD
A;Experimental source: var. tenebrionis
R;Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.
Mol. Microbiol. 14, 381-389, 1994
A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized strain
A;Reference number: S60781; MUID:95131759; PMID:7830581
A;Accession: S60781
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-652 <ADA>
A;Cross-references: UNIPARC:UPI000002B8CD; EMBL:U10985; NID:g506182; PIDN:AA43266.1; PIDN:AA43266.1; PIDN:AA43266.1
A;Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Wu, S.J.; Dean, D.H.
J. Mol. Biol. 255, 628-640, 1996
A;Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis
A;Reference number: S62317; MUID:96163559; PMID:8568902
R;Donovan, W.P.; Gonzalez, J.M.
Mol. Gen. Genet. 214, 365-372, 1988
A;Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis
A;Reference number: I39812; MUID:89112139; PMID:3146015
A;Accession: I39812
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 9-652 <RES>
A;Cross-references: UNIPARC:UPI000002B8CD; GB:h37207; NID:g142735; PIDN:AA50255.1; PIDN:AA50255.1; PIDN:AA50255.1
A;Experimental source: strain EG2158
R;Teixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.
J. Bacteriol. 175, 2952-2960, 1993
A;Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a
A;Reference number: I39813; MUID:93259939; PMID:8491716
A;Accession: I39813
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 9-58 <RES>
A;Cross-references: UNIPARC:UPI00000B007B; GB:L03393; NID:g304150; PIDN:AAA2350.1; PIDN:AAA2350.1; PIDN:AAA2350.1
C;Genetics:
A;Gene: cryIIIA
A;Superfamily: Parasporeal crystal protein
C;Keywords: delta-endotoxin

Query Match 15.9%; Score 620.5; DB 2; Length 652;
Best Local Similarity 26.9%; Pred. No. 3.2e-31;
Matches 198; Conservative 109; Mismatches 302; Indels 127; Gaps 28;

QY 1 MNQNNNEYEII--DSKNLSPVSRNIDHSRYPTNNPQNTNYKELWLMCOGNTQYG 59
DB 9 MNPNNRSEHDTIKTENNEVPTN---HVQYPLAETNPNTLDLNYKEFLRWMTADN--- 60

QY 60 DNEPTASADTIAVSAAGTVSGTLLAGIGLTSISGPIGIIAIIISFGTLITVFWPAG 119
DB 61 -NTEALDSSTTKDVIQKISVWGDLGVG-----PPFG--GALVSFTYNTLNTIWPSE 111

QY 120 EQDKTVMQTKMGEIFVDPTLETESIKQLKLTLEGFRQLQSNTALDDWRKLRLOAP 179
DB 112 DP-----WKAFMEQVEALMDQKIADYAKNKAELQGLQNNVEDYVSALSSWQK----- 160

QY 180 GLPPSSALQQAALTILKIRFENVNDFTREIPGQLEYTKTLPIYQAQANFHLNLLQOG 239
DB 161 -NPVSSRNPSQGRIRLEFSAQSHFRNSMPSFAISGYEVLFTTYAQAANTHLLKDA 219

QY 240 AELADEW---NADHPSQIEFNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNEP 296
DB 220 QIYGEENGVEKEDI-----AEFYKRLQKLTQETDHCVKWYVGLDKLRGSSY 267

QY 297 MRWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKTELTRFIYTTTEINFDR 356
DB 268 ESMVNFNRYREMTLVLDLIALFLPYDLVRLPKS-----VKTELTRDVLTDPI----- 316

QY 357 TYLEIQPNLAIMEYNLTRSGL-----RLFSFLDELIFYTKNET--YGNRLVGIANRNR 407
DB 317 ----VGVN-NLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYGVGDSNFYWSGNY 371

QY 408 -STVATTG-----TEIYGBRTGPTTKTLIPES-YKVSIVTDROVTPSPFNIFTI 460
DB 372 VSTRPSIGSNDIITSPYGNKSSEPQVNFKEKVRVAVANTNLAWPSA-----VTSGV 427

QY 461 NQIELYLNNSPSNKL---TVSAGNLSNDKTTDFQFPVKCKDCKPIINPNCLPSYNSYSH 517
DB 428 TKVEFSQYNDQTDSEASTQTYDSKRNVGAVSWDSIDQLPPETTDBLEK----- 475

QY 518 ILSQFSLFNYSYKIGIALNLTLYTGALG-----WTHSSVNRNNAISDKITMTIPAIKNS 571
DB 476 -----GYSHQLNVMCFMQSGRTIPVLVTHKSVDFNMIDSKKITQLPLVKAYK 527

QY 572 LDTNSKVIIEGPGHTGNNLVYLSQGRLEITCRTP--NSTQSYIIRLAYATNGAGNTLPNI 629
DB 528 LQSGASVAGPRTGGDIIIOCTENGSAATIVTPDVSYQYRARIHYASTS-----QI 581

QY 630 SLTIPGVIGIPPORLANNFTSGTNYN---NLQYGDGFGYFQFPFSTVTLPLNRNIPFIFNRAD 686
DB 582 TFTL-SLDGAP---FNQYFDPKTIKNGDTLTYSNFNLSASTPELSEGN-NLQIGVTGLS 636

QY 687 VNSIILIDKIEFIP 702
DB 637 AGDKV-YIDKIEFIPV 651

RESULT 11

S00873

Parasporeal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporeal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C;Accession: S00873

R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:g40264; PIDN:
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
A;Superfamily: Parasporeal crystal protein
C;Keywords: delta-endotoxin

Query Match 15.6%; Score 611; DB 2; Length 1228;
Best Local Similarity 26.2%; Pred. No. 3.3e-30;
Matches 210; Conservative 113; Mismatches 294; Indels 184; Gaps 35;

QY 1 MNQNNNEYEII--DSKNLSPVSRNIDHSRYPTNNPQNTNYKELWLMCOGNTQYG 60
DB 1 MTSNRKNNEIINA-----VSNHSAQMDLLP-----DARIEDSLCIAEGN----- 40

QY 61 NEPTASADTIAVSAAGTVSGTLLAGIGLTSISGPIGIIAIIISFGTLITVFWPAGE 120
DB 41 NIDPFVSAST---VQTGINIAGRILGVIG-----VPPAGQLASFSYFLVGLMWRGR 89

QY 121 QDKTVMQTKMGEIFVDPTLETESIKQLKLTLEGFRQLQSNTALDDWRKLRLOAP 180
DB 90 DQ---WEIPLFHVQLINQIITENARTALARLQGLGDSFRAYQOSLEDMLE-----NRDD 142

QY 181 LPSSALQQAALTILKIRFENVNDFTREIPGQLEYTKTLPIYQAQANFHLNLLQOGA 240
DB 181 LPSSALQQAALTILKIRFENVNDFTREIPGQLEYTKTLPIYQAQANFHLNLLQOGA 240

Db 143 ARTSRVLYTQYIALEL-----DFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDAS 195
QY 241 ELADENNADHPQIEPNAGTSD---YKLLKENIPKYSNYCANTYREGNKLNRPENM 297
Db 196 LFGSEFGL-----TSQEIQRYYERQVTRDYSYDVCVEYNTGLNSLRGTAA 243
QY 298 RWSIFNDYRRYMTITVLDITTAQSFYDIKRYKDSIGRIGGIKT-----TEIN 352
Db 244 SWRYNQPRDLTLGLDLVALPSPYDTRYPIN-----TSQALTREYVTDIGAATGN 297
QY 353 FDLRT-YLEIQPNLAIMEYNLTRSGLRFLPSFLDEL-IF-----YTKNETYGN 397
Db 298 MASMNWYNNAPSAIAAAIRSP-HLLDFLEQLTIFGSASSRWSNTRHMTYWRGHTIQS 356
QY 398 RLVGIANRRTVATTGTETIYGERGTPPT-----TKTLIPFESYKYSIVTDROVTPSP 453
Db 357 RPIG-GLGNTSTHGATNTSI-----NPVTLRPSARDVYRTESYAGVLLMGYLEIPHG 409
QY 454 PNIYFTINQIELYLNNSPKLTYSGAGNLSNDKTTDFQPVK-----KCKPPIPN 507
Db 410 PTVRFNF-----TNPN-----ISRGTANYSQPYESPLQLKQSETLPPE 451
QY 508 CL--PSYNSYSHLSQFLSNYSYKIGLALNI-LYTGALGWTSHSSVNRNNAISDKIITMI 564
Db 452 TTERPNYESYSHLSHIGIILQS-----RVNVPVYS-----WTHRSADRTNTIGPNRITQI 502
QY 565 PAIKGNSLDTNSKVIKSGPHTGGLNVLVLSQ-----GRLEITCRTPNSTQSYIIRLYAT-- 619
Db 503 PMVKASLPQGTTVVRPGPGTGDIILRRNTTGGFGPIRVTVNGP-LTORIRIGFRYASTV 561
QY 620 -----NGAGNTLPNISLTIPGVIGIPPPORLNTTSGTNNLYQDGFYFQPPSTVTL 673
Db 562 DFDFFVSRGGTTVNNFRF-----LRTMNSG-----DELKGNFVRRAFTT----- 601
QY 674 LNRNPIPFNR-ADV-----SNSILIIDKIEPIPTSSVRQNRKQKLETIQTKIN 723
Db 602 -----PFTTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVATPEAYD---LERAQEA 653
QY 724 TPTNTKTKTLNTEATNYDID 744
Db 654 ALFTNTPRRLKTDVTDYHID 674

RESULT 12
I39815
insecticidal protein cryV - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39815
R:Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
iensis subsp. kurstaki.
A:Reference number: I39815; MUID:93298009; PMID:8517758
A:Accession: I39815
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:g142767; PIDN:
C:Genetic:
A:Gene: cryV
C:Superfamily: Parasporal crystal protein

Query Match 15.1%; Score 588.5; DB 2; Length 719;
Best Local Similarity 26.1%; Pred. No. 3.9e-29;
Matches 207; Conservative 112; Mismatches 293; Indels 181; Gaps 34;

QY 15 KNLSYPSNRNIDH-SRYPYTNPNQPLQNTNYKEWLNMCQNTQYQDGFETASADTIAA 73
Db 8 KHQSFSSNAKVDKISTDSLKNETDIELQNINHDCLM-----SEY-ENVEPFPVASTIQ- 61
QY 74 VSAGTIVSGTLLAGIGLTSISGFIGI--IGAIISFGTLITVFWPAGEQDKTVTQFIK 131

Db 62 -----TGIGIAGKILGTGLVPPAGQVASLYSFILGELWPKG---KNQWEIFME 106
QY 132 MGEIFVDPTLTSIIKQLKLTLEGFRQILQSYNTALDDW---RKLKRLQAPGLPPSSALQ 188
Db 107 HVEEIIQKISTYARNKALTDLKGLGDALAVYHDSLESWVGVRNNTRAR-----SVVK 159
QY 189 QAALTILKIRFENVHNDFIREFIOLETYKTLPIYAQAANFHLNLLCOGAELADEWNA 248
Db 160 SQYIALEM-----FVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKENG- 211
QY 249 DIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLNRPENMNRSIFNDYRY 308
Db 212 -LSSSEI-----STFYNRQVERAGDYSCHVKVYSTGLNLRGTNAESVRYNQFRRD 263
QY 309 MTITVLDITTAQSFYDIKRYKDSIGRIGGIKT--ELTREIYYTEI-----NFDRLT-Y 358
Db 264 MTLMLDLVALPSPYDTRYPIN-----IKTAQLTREYVTDIGAIVPHPSFTSTTWY 315
QY 359 LEIQPNLAIMEYNLTRSGLRFLPSFLDELIFYT-----KNETYGN-----RLVGIAN 404
Db 316 NNNAISPSAIEAAVVRNP-HLLDFLEQVTIYSLLSRWSNTQYNNMWGGHKLERTIG-GT 373
QY 405 RNRSTYATTGTETIYGERGTPPTTKLIPPE-----YKVSIVTDROVTPSP---FPNIYF 458
Db 374 LNISTQGSTNTSI-----NPVT---LPFTSRDVRTESLAGLNLFLTQPVNGVPRVDF 423
QY 459 TINQIELYLNNSPKLTYSGAGNLSNDKTTDFQPVKCKPPIPNCLPSYNSYSHI 518
Db 424 ---HWKFVTHPIASNFFYPGYAGITQIQDSENELPPEATGQ-----PNYESYSHR 472
QY 519 LSQFLSNYSYKIGLALNITYTGALGWTSHSSVNRNNAISDKIITMIPAIKNSLDTNSKV 578
Db 473 LSHIGLISASHKALVYS-----WTHRSADRTNTIEPNSITQIPLVKAFLNSGA 524
QY 579 IEGPHTGGLNVLVLSQ-----RLEITCRTPNSTQSYIIRLYAT-----NGAG 623
Db 525 VRPGFTGGDIILRRNTTGTGDIRVNI---NPPAQRYVRIRYASTTDLQFHTSINGKA 581
QY 624 NTLPLNISLTIPGVIGIPPPORLNTTSGTNNLYQDGFYFQPPSTVTLPLNRNIPFIN 683
Db 582 INQGNFSATM-----NRGEDLDYKTFRTVGFTT-----PFSP- 613
QY 684 RADVSNILI-----IDKIEPIPTSSVRQNRKQKLETIQTKINTPFTNHTK 731
Db 614 -LDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYEYD---FEKAQEKVTLFTSTNP 669
QY 732 NTLNTEATNYDID 744
Db 670 RGLKTDVKDYHID 682

RESULT 13
I39814
insecticidal protein cryVI - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39814
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I39814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPARC:UPI0000036009; GB:L36338; NID:9540281; PIDN:AAC36999.1; PID:
C:Genetic:
A:Gene: cryVI
C:Superfamily: Parasporal crystal protein

Query Match 15.0%; Score 585.5; DB 2; Length 719;
Best Local Similarity 26.1%; Pred. No. 6e-29;

A;Cross-references: UNIPROT:Q45752; UNIPARC:UPI000002DB73; EMBL:X62821; NID:G40289; PDB:1Y29

C;Genetics: A:Gene: cryu C:Superfamily: Paraaporal crystal protein C;Keywords: delta-endotoxin

Query Match 15.0%; Score 585.5; DB 2; Length 719;
Best Local Similarity 26.1%; Pred. No. 6e-29;
Matches 207; Conservative 111; Mismatches 294; Indels 181; Gaps 34;

Qy 15 KNLSYSPNRNIDH-SRYPYTNPNQPLONTNYKEWLNMCQGTQYQDGFETPASADTIAA 73
Db 8 KHOSFSSNAKVDKISTDSLKNETDIELONINHHEDCLKM-----SEY-ENVEFPFVASTIQ- 61
Qy 74 VSAGTIVSGTLLAGIGGLTSGISPGIG--IGALLISFGTLITVFWPAGEQDKVTWQTFIK 131
Db 62 -----TGIGIAGKILGTGVPFAGQVASLYSPILGELWPKG---KNQWIFPME 106
Qy 132 MGEIFVDPPTESIKQLKQLTSGFQRIQLQSYNTALDDW---RKLKRLQAPGLPPSSALQ 188
Db 107 HVBEIINQKISTYARNKALTDLKGGLDALAVYHDSLESVWGNRNTRAR-----SVVK 159
Qy 189 QAALTALKIRENVHNDIFIREPGFQLETYKTLPIYAQANFHLNLOQGAELADBNWA 248
Db 160 SQVIALELM-----FVQKLPSFAVSGSEVPLPIYAQANHLHLLLDASIFGKEWG- 211
Qy 249 DIHPSQETPNAGTSDDYKYLLKENIKPYSNYCANTYREGLNKLNEPNRWSIFNDYRRY 308
Db 212 -LSSEI-----STFYNQVERAGDYSVHCVKWTSTGLNNLRGTNAESWVRYNQFRD 263
Qy 309 MTITVLDTTAQSFYDIKRYKDSIGRIGIKT--ELTREIYITEI-----NFDRLT-Y 358
Db 264 MTMLVLDLVALFPSTQMYP-----IKTTAQLTREVIYDTAIGTVHPHPSTSTTWY 315
Qy 359 LEIQPLNLAIMEYNLTRSGLRLPFLDELIFYT-----KNETYGN-----RLYCIAN 404
Db 316 NNWAPFSALAAVVRNP-HLLDFLQVITYLLSRWSNTQYNNMGGHKLEPRTIG-GT 373
Qy 405 RNRSTVATTGTEIYGERTGPPTKTLIPFES---YKVSIVTDRQVTTTSP---FPNIYF 458
Db 374 LNIQTQGSTWTSI-----NPVT---LPFTSRDVTSTESLAGLNLFLOPVNGVPRVDF 423
Qy 459 TINQIELYLNNSPNKLYTSAGGNLNDKTTDFQPVKKDCKPIINPNCPLPSYNSYSHI 518
Db 424 ---HWKFVTHPIASDNFFYPYAGIGTQLQDSNELPPEATGQ-----PNYESYSHR 472
Qy 519 LSQFSLFNYSYKIGLALNILYTCALGWTHSSVNRNNAISDKIITMIPAIGNSLSDTNSKV 578
Db 473 LSHGILISASHVVALVYS-----WTHRSADRTWIEPNSITQIPLVKAFLNSGAAV 524
Qy 579 IEGFGHTGGNLYLOSQG-----RLBITCRTPNSTQSYVIRLRYAT-----NGAG 623
Db 525 VRGFGFTGGDILARTNTGTFTGDIRVNI---NPPFAQRYRVIRYASTDLOFHTSINGKA 581
Qy 624 NTLPLNLSLITPGVIGIPQRLNNTFSGTYNNLLOYGDFGYFQFPSTVTPLPLRNIPIFIN 683
Db 582 INQGNFSATM-----NREGDLDYKTFRTVGFTT-----PFSP- 613
Qy 684 RADVNSILI-----IDKIEFTIPITSSVRQNRKQKLETIQTIKNTFFNTHTK 731
Db 614 -LDVQSTFTIGAWNFSGSEVNIIDRELFVPVEVYEAED---FEKAQEKVATLFTSTNP 669
Qy 732 NTLNIEATNYDID 744
Db 670 RGLKTDVKDYHD 682

RESULT 15
JH0261
parasporal crystal protein cry3Ca1 - *Bacillus thuringiensis* subsp. *kurstaki* (strain BT11 N)
Alternate names: parasporal crystal protein cryIIID
C/Species: *Bacillus thuringiensis* subsp. *kurstaki*
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 05-Oct-2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:47:28 ; Search time 47 Seconds
(without alignments)
1308.738 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYEIIDSKNLSYP.....FFTHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCPUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	29.5	1180	2	US-09-224-024-28
2	1153	29.5	1180	4	PCT-US94-07902-28
3	900	23.0	686	2	US-09-224-024-31
4	900	23.0	686	4	PCT-US94-07902-31
5	791.5	20.3	1169	1	US-08-315-468-4
6	710	18.2	651	1	US-08-315-468-6
7	710	18.2	651	2	US-07-941-650A-4
8	710	18.2	659	2	US-08-996-441B-112
9	710	18.2	659	2	US-08-993-722A-112
10	710	18.2	659	2	US-08-993-170A-112
11	710	18.2	659	2	US-08-993-775B-112
12	710	18.2	659	2	US-09-427-770-112
13	710	18.2	659	2	US-09-427-769-112
14	704	18.0	652	2	US-08-996-441B-110
15	704	18.0	652	2	US-08-993-722A-110
16	704	18.0	652	2	US-08-993-170A-110
17	704	18.0	652	2	US-08-993-775B-110
18	704	18.0	652	2	US-09-377-466B-4
19	704	18.0	652	2	US-09-427-770-110
20	704	18.0	652	2	US-09-427-769-110
21	704	18.0	652	2	US-10-232-665-4
22	704	18.0	652	4	PCT-US92-00040-2
23	697	17.8	652	2	US-09-377-466B-6
24	697	17.8	652	2	US-10-232-665-6
25	695	17.8	652	2	US-08-996-441B-4
26	695	17.8	652	2	US-08-996-441B-10
27	695	17.8	652	2	US-08-996-441B-28

28	695	17.8	652	2	US-08-996-441B-44	Sequence 44, Appl
29	695	17.8	652	2	US-08-996-441B-68	Sequence 68, Appl
30	695	17.8	652	2	US-08-996-441B-98	Sequence 98, Appl
31	695	17.8	652	2	US-08-996-441B-111	Sequence 111, Appl
32	695	17.8	652	2	US-08-993-722A-4	Sequence 4, Appl
33	695	17.8	652	2	US-08-993-722A-10	Sequence 10, Appl
34	695	17.8	652	2	US-08-993-722A-28	Sequence 28, Appl
35	695	17.8	652	2	US-08-993-722A-44	Sequence 44, Appl
36	695	17.8	652	2	US-08-993-722A-68	Sequence 68, Appl
37	695	17.8	652	2	US-08-993-722A-98	Sequence 98, Appl
38	695	17.8	652	2	US-08-993-722A-111	Sequence 111, Appl
39	695	17.8	652	2	US-08-993-170A-4	Sequence 4, Appl
40	695	17.8	652	2	US-08-993-170A-10	Sequence 10, Appl
41	695	17.8	652	2	US-08-993-170A-28	Sequence 28, Appl
42	695	17.8	652	2	US-08-993-170A-44	Sequence 44, Appl
43	695	17.8	652	2	US-08-993-170A-68	Sequence 68, Appl
44	695	17.8	652	2	US-08-993-170A-98	Sequence 98, Appl
45	695	17.8	652	2	US-08-993-170A-111	Sequence 111, Appl

ALIGNMENTS

RESULT 1
US-09-224-024-28
; Sequence 28, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Leslie Hickie
; APPLICANT: Jewel Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-224-024-28

Query Match 29.5%; Score 1153; DB 2; Length 1180;
Best Local Similarity 37.2%; Pred. No. 6.4e-89;
Matches 282; Conservative 131; Mismatches 282; Indels 64; Gaps 25;
Oy 5 NNNEYEIIDS--KNLSYPSNRNIDHSRYPTNPNPQPLQNTNYKEWLNMCQGTQYGDNF 62

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Db      6 NKNEYETLNASQKLNISNN-----YRYPLENSPKQLQSTNYKDWLNMCQOQYGGDF 61
QY      63 ETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db      62 ETPIDS---GELSAITVVGTLTGFGFT---PLGL---ALIGFTLIPVLFPQAQDOS 111
QY      123 KTWMTQFIKMGEIFVDTPLETESI KQLQTLGSGFRQILQSNTALDDWRKLKELQAPGLP 182
Db      112 NT-WSDFITQTKNIITKKEIASTYISNANKILNRSFNVIYTHNHLKTWE-----NNPNPQ 165
QY      183 PSSALQQAALTLKIRFENVHND FIREIP--GFQLETYKTLTLLPIYAAQANFHLNLQOGA 240
Db      166 NTQDVRTQIQLVHYHFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANLHLTVLNQAV 225
QY      241 ELADENADIHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKKGLNLKTTDPSNLD 284
QY      296 -NMRWSIENDRYRYMTITVLDTIAQSFVDIKRYKDSIGRIGIKITELTREIYTTINPD 354
Db      285 GNINWNTYTYRTKMTTAVLDLVALFPNDVGKPI-----GVQSELTREIYQV-LNFE 337
QY      355 RLTYLEIOPNLAIMBYNLTGRSLRFLSFLDELIFFTKNETYGNRLVGIANRNRSTYA---411
Db      338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQOTTPNPF--TSHYNMFHYTLDN 393
QY      412 TTGTEIIGERTGPPTTKTLIPESYKVSIVTDQVTPSPPNYIYFTTINQIELYLNNSP 471
Db      394 ISQKSSVFGNNHVTDKLSL--GLATNIYIFLLNVISLDNKLNDYNNISKMDFFITNGT 451
QY      472 ---SNKLTYSAGNLSNDKKTTFDQFPVKCKPPIINPNCLPSYNSYSHILSQFSLFNY- 527
Db      452 RLLEKELT-AGSGQITYDVNKNIFGLPIKPRENQAIPFLPTFYDNYSHILSFIKSLSP 510
QY      528 -SYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGPGHTG 586
Db      511 ATYK-----TQVYTFE--WTHSSVDPKNTIYTHLTQIPAVKANSIGTASKKVQGPHTG 563
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RESULT 2
PCT-US94-07902-28
; Sequence 28, Application PC/TUS9407902
; GENERAL INFORMATION:
; APPLICANT: Street address: 4980 Carroll Canyon Road
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030
; APPLICANT: Telex number:
; TITLE OF INVENTION: Materials and Methods for the Control of
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
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; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07902
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07902-28

Query Match      29.5%; Score 1153; DB 4; Length 1180;
Best Local Similarity 37.2%; Pred. No. 6.4e-89;
Matches 282; Conservative 131; Mismatches 282; Indels 64; Gaps 25;

QY      5 NKNEYETLNASQKLNISNN-----YRYPLENSPKQLQSTNYKDWLNMCQOQYGGDF 62
Db      6 NKNEYETLNASQKLNISNN-----YRYPLENSPKQLQSTNYKDWLNMCQOQYGGDF 61
QY      63 ETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db      62 ETPIDS---GELSAITVVGTLTGFGFT---PLGL---ALIGFTLIPVLFPQAQDOS 111
QY      123 KTWMTQFIKMGEIFVDTPLETESI KQLQTLGSGFRQILQSNTALDDWRKLKELQAPGLP 182
Db      112 NT-WSDFITQTKNIITKKEIASTYISNANKILNRSFNVIYTHNHLKTWE-----NNPNPQ 165
QY      183 PSSALQQAALTLKIRFENVHND FIREIP--GFQLETYKTLTLLPIYAAQANFHLNLQOGA 240
Db      166 NTQDVRTQIQLVHYHFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANLHLTVLNQAV 225
QY      241 ELADENADIHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTTYKKGLNLKTTDPSNLD 284
QY      296 -NMRWSIENDRYRYMTITVLDTIAQSFVDIKRYKDSIGRIGIKITELTREIYTTINPD 354
Db      285 GNINWNTYTYRTKMTTAVLDLVALFPNDVGKPI-----GVQSELTREIYQV-LNFE 337
QY      355 RLTYLEIOPNLAIMBYNLTGRSLRFLSFLDELIFFTKNETYGNRLVGIANRNRSTYA---411
Db      338 ESPYKY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQOTTPNPF--TSHYNMFHYTLDN 393
QY      412 TTGTEIIGERTGPPTTKTLIPESYKVSIVTDQVTPSPPNYIYFTTINQIELYLNNSP 471
Db      394 ISQKSSVFGNNHVTDKLSL--GLATNIYIFLLNVISLDNKLNDYNNISKMDFFITNGT 451
QY      472 ---SNKLTYSAGNLSNDKKTTFDQFPVKCKPPIINPNCLPSYNSYSHILSQFSLFNY- 527
Db      452 RLLEKELT-AGSGQITYDVNKNIFGLPIKPRENQAIPFLPTFYDNYSHILSFIKSLSP 510
QY      528 -SYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGPGHTG 586
Db      511 ATYK-----TQVYTFE--WTHSSVDPKNTIYTHLTQIPAVKANSIGTASKKVQGPHTG 563
QY      587 GNLVYLSQGRLEITCRTPNSTQSYIRLYRYATNGAGNTLPNLSLTIPGVIGIPPORLNN 646
Db      564 GDLI--DPKDFKITCOHSNFQOQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
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QY 569 GNSLDTNSKVIIEGPGHTGNNLVLO-----SQGLEITCTPNSQTOSYIYRLRYATNGAGN 624
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QY 625 TLPNLSITIPGVIGIPQRLNNTFSGTNNVNNLOY--GDFGY--FQPPSTVTLPLNRNIPF 680
Db 576 --TNLRLFV-----QNSNDFLVIYINKTNWIDGDLTYQTFDFATS-----NSNMGF 620
QY 681 IFNRAD-----VNSILIIIDKIEFIPI 702
Db 621 SGTNDNFIIGAESFVSNKIIYIDKIEFIPV 650

RESULT 7

US-07-941-650A-4
; Sequence 4, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Uveda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
; FILING DATE: 21-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: tolworthi
; INDIVIDUAL ISOLATE: 43f
; IMMEDIATE SOURCE:
; CLONE: E. coli XL1-Blue (pML98-4), NRRL B-18291
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..651
; US-07-941-650A-4

Query Match 18.2%; Score 710; DB 2; Length 651;
Best Local Similarity 28.9%; Pred.No.1.4e-51;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;
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Db 1 MNPNNRSEYDTIKVTPNSLPTN---HNQYPLADNPNSTLEELNYKEFLRMTADNST--54
QY 60 DNFETPASADTTAAVSAGTIVSGTLLAGIGGTSISGPIGIIGAIISFGTLITVFWPAG 119
Db 55 ---EVLDSSTVADAVGTGTSVVGQILGVVG-----VFFAGALTSFYQSFLNALWPS-102
QY 120 EODKTVMTOFIKMGIFVDTPLTESIKQLKQTLQLEGFRQILQSYNTALDDWRKLKELQAP 179
Db 103 --DADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDVYNALOSWK-----153
QY 180 GLPPSSALQQAALTLKIRPENVNDFIRIPGQLETYKTLTLLPIYAQAANFHLNLLQOG 239
Db 154 -APVNLRSRSDRINELFSQAESHFRNSMPSPAVSKFEVLFLPTVAQAANTHLLLLKDA 212
QY 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKSYNCANTYREGLNKLNENPN 296
Db 213 QVFGGEWGY-----SSEDAIEFYQRLKLTQYTDHCVMVNVNGLSLRGSTY 260
QY 297 MEWSIFNDYRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELTRYITTEINFDR 356
Db 261 DAWKFNRRREMTLTVLDLIVLFPFYDVRLLYSK-----GVKTELTRDIFDPI-FTLN 313
QY 357 TYLEIQPNLAIMEYNLTRSGRLFSGLDELIFYTK-----NETYGNRLVGIANR 405
Db 314 ALQEVGPTFSSIENSIRKP--HLFDYLRGIEFHTRLRPGVSGKDSFNYWSGNY---VETR 368
QY 406 NRSTYATTCTEIIYERTGPTTKLIPESKVSIVTDROV--TPTSFPFN--IYFTIN 461
Db 369 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQKVY---RTIANTDIAAFFDQGIYFGVT 422
QY 462 QIELYLNNSPNKL---TVSA-----GGNLSNDK---KTTFDQFPVKKDKCKPIINPC 508
Db 423 KVDFSQYDDQKNETSTQTYDSKRYNGYLGAQOSIDQLPETTD--EPLSK-----470
QY 509 LPSYNSYSHLSQFSLFNYSYKIGLALNLYTGALGWTHSSVNRNNAISDKIITMIPA 568
Db 471 -----AYSHQLNVAECFLMQDRRGIT--PFFT---WTHRSVDFTNTIDAEKITQLPVVK 519
QY 569 GNSLDTNSKVIIEGPGHTGNNLVLO-----SQGLEITCTPNSQTOSYIYRLRYATNGAGN 624
Db 520 AYALSSGASIIIEGPGTGGNLLFLKSSNSIAKFKVTLNSAALLQRYRVRIRYAST-----575
QY 625 TLPNLSITIPGVIGIPQRLNNTFSGTNNVNNLOY--GDFGY--FQPPSTVTLPLNRNIPF 680
Db 576 --TNLRLFV-----QNSNDFLVIYINKTNWIDGDLTYQTFDFATS-----NSNMGF 620
QY 681 IFNRAD-----VNSILIIIDKIEFIPI 702
Db 621 SGTNDNFIIGAESFVSNKIIYIDKIEFIPV 650

RESULT 8

US-08-996-441B-112
; Sequence 112, Application US/08996441B
; Patent No. 6023013
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Brussock, Susan M.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Terssch, Michael A.
; APPLICANT: Romano, Charles
; TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS


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Db 63 ---EVLDSSTVKDVGTSVWGQILGWG-----VPPAGALTSFYQSPFLNAINWPS- 110
Qy 120 EQDKTWTQIKMGEIFVDTPLETISKQLQTLQLEGFRQILOSYNTALDDWRKLKQLAP 179
Db 111 --DADPWKAFMAQVEVLIDKKIEYAKSKALAELOQLNNFEDYVNALDSWK- 161
Qy 180 GLPPSALQQAALTUKIRFENVHNDPIREIPGFOLEYTKTLPIYAQAANFHLNLQOG 239
Db 162 -APVNLRSRQDRIRLEFSQAESHFNMPSPFAVSKFEVLFTPTTAAQANTHLLLLKDA 220
Qy 240 AELADEWADIHPSQIEPNAGTSD--YYKLAKENIPKYSNYCANTYREGNKLKRNPN 296
Db 221 QVFGSEWGY-----SSEDIAEFYQRLKLTQQYTDHCYVNVNGLSLAGSY 268
Qy 297 MRWSIFNDYRRYMTIVLDTIAQFSYDIKRYKDSIGRIGGKTELTRRIYITEINFDRL 356
Db 269 DAWVKFNFRREMTLVLDLIVLPPFDVRLYSK-----GVKTELTRDIFTDPI-FTLN 321
Qy 357 TYLEIOPNLAIMYNLTRSGRLPFLDELIFVTK-----NETYGNRLVGIANR 405
Db 322 ALQEGYPTFSSIENSIRKP--HLFDYLRGIEPHTRLRPGYSGKDSFNWWSGNY---VETR 376
Qy 406 NRSTYATTGTEIYIGERTGPPTTKLIPFESYKVSIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQVY---RTIANTDIAAFPDKGIYFVGT 430
Qy 462 QIELYLNNSPNKL---TVSA-----GGNLSNDK---KTDFQFPVKCKCKPIINPNC 508
Db 431 KVDQSYDDQKNETSTQYDSKRYNGYLGAQDSIDLPPETD--BPLEK----- 478
Qy 509 LPSYNSYSHILSQSLFNYSYKIGLALNLTGALGTHSSVNRNNAISDKIITMIPAK 568
Db 479 -----AYSHQLNVAECFLMQDRGTI--PPFT-----WTHRSVDFNTIDAETKIQLPVVK 527
Qy 569 GNSLDTNSKVIIEPGHGTGNLVYQ-----SQGRLEICTRPNSTQSYIRLRYATNGAGN 624
Db 528 AYALSSGASIIIEGPGTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYAST--- 583
Qy 625 TLNLSLTIPGVIGIPQRLNNTFSGTNNYLOQ--GDFGY--FQFPSTVTLPLNRNIPF 680
Db 584 --TNLRLFV-----QNSNNDFLVIYINKTMNIDGLTYQTFDFATS-----NSNMGF 628
Qy 681 IFNRAD-----VNSILIIDKIEFIPI 702
Db 629 SGTNDFIAGSFVSNKIIYIDKIEFIPV 658
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RESULT 10

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US-08-993-170A-112
; Sequence 112, Application US/08993170A
; Patent No. 6063597
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Bruesock, Susan M.
; APPLICANT: Malvar, Thomas W.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Tersch, Michael A.
; TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO
; TITLE OF INVENTION: COLEOPTERAN INSECTS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,170A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-170A-112

Query Match 18.2%; Score 710; DB 2; Length 659;
Best Local Similarity 28.9%; Pred. No. 1.5e-51;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;

Qy 1 MNQNNNEVEIID-SKNLSYSPSNRNIHDSRYPTNNPQLONTNYKEWLNWCOGNTQYG 59
Db 9 MNPNNRSEYDTTKVPSNSELPTN----HNQYPLADNPSTLBELNYKEFLRTADNST-- 62
Qy 60 DNFETPASADTTAAVSAGTIVSGTLLAGIGLTSISGPITGICAILISFGTLITVFWPAG 119
Db 63 ---EVLDSSTVKDVGTSVWGQILGWG-----VPPAGALTSFYQSPFLNAINWPS- 110
Qy 120 EQDKTWTQIKMGEIFVDTPLETISKQLQTLQLEGFRQILOSYNTALDDWRKLKQLAP 179
Db 111 --DADPWKAFMAQVEVLIDKKIEYAKSKALAELOQLNNFEDYVNALDSWK- 161
Qy 180 GLPPSALQQAALTUKIRFENVHNDPIREIPGFOLEYTKTLPIYAQAANFHLNLQOG 239
Db 162 -APVNLRSRQDRIRLEFSQAESHFNMPSPFAVSKFEVLFTPTTAAQANTHLLLLKDA 220
Qy 240 AELADEWADIHPSQIEPNAGTSD--YYKLAKENIPKYSNYCANTYREGNKLKRNPN 296
Db 221 QVFGSEWGY-----SSEDIAEFYQRLKLTQQYTDHCYVNVNGLSLAGSY 268
Qy 297 MRWSIFNDYRRYMTIVLDTIAQFSYDIKRYKDSIGRIGGKTELTRRIYITEINFDRL 356
Db 269 DAWVKFNFRREMTLVLDLIVLPPFDVRLYSK-----GVKTELTRDIFTDPI-FTLN 321
Qy 357 TYLEIOPNLAIMYNLTRSGRLPFLDELIFVTK-----NETYGNRLVGIANR 405
Db 322 ALQEGYPTFSSIENSIRKP--HLFDYLRGIEPHTRLRPGYSGKDSFNWWSGNY---VETR 376
Qy 406 NRSTYATTGTEIYIGERTGPPTTKLIPFESYKVSIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTITSPFYGDKSIEPIQK--LSPDGQVY---RTIANTDIAAFPDKGIYFVGT 430
Qy 462 QIELYLNNSPNKL---TVSA-----GGNLSNDK---KTDFQFPVKCKCKPIINPNC 508
Db 431 KVDQSYDDQKNETSTQYDSKRYNGYLGAQDSIDLPPETD--BPLEK----- 478
Qy 509 LPSYNSYSHILSQSLFNYSYKIGLALNLTGALGTHSSVNRNNAISDKIITMIPAK 568
Db 479 -----AYSHQLNVAECFLMQDRGTI--PPFT-----WTHRSVDFNTIDAETKIQLPVVK 527
Qy 569 GNSLDTNSKVIIEPGHGTGNLVYQ-----SQGRLEICTRPNSTQSYIRLRYATNGAGN 624
Db 528 AYALSSGASIIIEGPGTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYAST--- 583
Qy 625 TLNLSLTIPGVIGIPQRLNNTFSGTNNYLOQ--GDFGY--FQFPSTVTLPLNRNIPF 680
Db 584 --TNLRLFV-----QNSNNDFLVIYINKTMNIDGLTYQTFDFATS-----NSNMGF 628
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QY 681 IFNRAD-----VNSILIIDKIEPIPI 702
DB 629 SGTNDFTIIGAESFVSNEKIYIDKIEPIPV 658

RESULT 11
US-08-993-775B-112
; Sequence 112, Application US/08993775B
; Patent No. 6077824
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Brussock, Susan M.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Tersch, Michael A.
; TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF
; TITLE OF INVENTION: DELTA-ENDOTOXINS AGAINST INSECT PESTS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,775B
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO.150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 659 amino acids
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-993-775B-112

Query Match 18.2%; Score 710; DB 2; Length 659;
Best Local Similarity 28.9%; Pred. No. 1.5e-51;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;

QY 1 MNQNNNEYEIID-SKNLSYSPNRNIDHSRYPTNNPNQPLONTNYKEWLNMCQNTQYG 59
DB 9 MNPNRSEYDIKVTPELSELPN-----HNQPLADNPNSTLEELNYKEFLRWADNST-- 62
QY 60 DNFEFTASADTAASAGTIYSGTLLAGIGGLTSISGPIGIGAIISFGTLITVFWPAG 119
DB 63 ---EVLDSSTVKDAVGTGSGVVGILGVVG-----VPPAGALTSPYQSFLNAWPS- 110
QY 120 EQDKVTWTOFTKMEIIFVDTPLTESIKOLKQTLQEGFRQILQSNYALDDWRKLRLOAP 179
DB 111 --DADPWKAFWAQVEVLIDKKIEEYAKSKALAEQLGLQNNFEDYVNALDSWKK----- 161
QY 180 GLPSSALQQAALTILKIRFENVHNDFIIEIPGFOLETYKTLILLPIYAQAANFHLNLLQOG 239
DB 162 -APVNLRRSQDRIRLELFSQAESHFRNSMPFVAFVFLPLPYAQAANTHLLLLKDA 220

QY 240 AELADEWNADIHPSQIEPNAGTSD-----YKLLKENIPKYSNYCANTYREGNLKLRNEPN 296
DB 221 QVGEEMGY-----SSEDIAEAFQORQLKLTQQYTDHCVMNVNVLNLSRGSTY 268
QY 297 MRNSIENDYRYMTITVLDIAQFSFYDIKRYKDSIGRIGIKTELREIYTTTINPDLR 356
DB 269 DAWVKFRFRREMTLTVDLILVLPFYDVRYSK-----GVKTELTRDIFTDPI-FTLN 321
QY 357 TYLEIQPNLAIMEYNLTRSGRLRFLSFLDELIFVTK-----NETYGNRLVGIANR 405
DB 322 ALQEVGYPTFSSIEANSIRKP--HLFDYLRGIEFHTLRAPGYSGKDSFNWGSNY---VETR 376
QY 406 NRSTYATGTIELIYGERTGPTTKTLIPFESYKSVIVTDROV--TPTSPPPN--IYFTIN 461
DB 377 PSIGSNDTITSPFYGDKSIEPIQK--LSFDGQKY---RTIANTDIAAFPDGKIYFGVT 430
QY 462 QIELYLNANSPSNKL---TYSA-----GGNLSNDK---KTTDFQFPVKDKCKPIINPNC 508
DB 431 KVDFSQYDDOKNETSTQTYDSKRYNGYLGAQDSIDQLPETTD--EPEK----- 478
QY 509 LPSYNSYSHILSQFSLFENYSYKIGLALNLYTGALGHTSHSVNRRNAISDKIITMIPA 568
DB 479 -----AYSHQNLVAECFLMQDRRCTI--PRFT-----WTHRSVDFENIDAETIQLPVK 527
QY 569 GNSLDTNSKVIIEGPGHTGGMVLYLQ-----SQGRLEITCRTPNSQSYVIRURYATNGAGN 624
DB 528 AYALSSGASITIEGPGFTGCGNLLFLKSSNSITAKFKVLNSAALLQRYVRIRYAST----- 583
QY 625 TLPNISLITPGVIGIPQRLNNTFSGTNNYLNQY--GDFGY--QFPSTVTLPLNRPFP 680
DB 584 --TNLRUFV-----QNSNDFLVYINKTNMIDGLTYQTDFATS-----NSNMGF 628
QY 681 IFNRAD-----VNSILIIDKIEPIPI 702
DB 629 SGTNDFTIIGAESFVSNEKIYIDKIEPIPV 658

RESULT 12
US-09-427-770-112
; Sequence 112, Application US/09427770
; Patent No. 6620988
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Brussock, Susan M.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Tersch, Michael A.
; APPLICANT: Romano, Charles
; TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
; TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/427,770
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/993,722
; FILING DATE: 18-DEC-1997
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APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terssch, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/993, 722A
APPLICATION NUMBER: US/08/993, 722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-722A-110

Query Match 18.0%; Score 704; DB 2; Length 652;
Best Local Similarity 29.0%; Pred. No. 4.7e-51;
Matches 217; Conservative 116; Mismatches 272; Indels 142; Gaps 32;
Qy 1 MNQNNNEVEIID-SKNLSVPSNRNIDHSVPYNNPNQPLQNTNWKELNMQ-QNTQY 58
Db 1 MNPNNRSEHTIKVTPNSELPTN-----HNQYPLADNPSTLEELNYKEFLRMTEDSSTEV 56
Qy 59 GDNFETPASADTIA-AVSAGTIVSGTLLAGIGGLTSGIPGIIIGAIISFGTLITVFWP 117
Db 57 LDN-----STVKDAVGTGIVVGVQLGVVG-----VPFAGALTSFYQSFLDTIMP 101
Qy 118 AGRODKTVTWTQFMGIEFVDTPLTESIKOLKLTLEGFRQIILQSNVNTALDDWRKLRQ 177
Db 102 S---DADPWAFMAQVEVLIDKIEEYAKSKALAEQLQGNFEDYVNALNSWK----- 153
Qy 178 APGLPSSALQQAAALTLLKIRFENVHNDFFIREIPGQLETVKTLTLLPIYAQANFHLNLLQ 237
Db 154 ---TPLSLRSQRDIREFLPSQAEHSFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLK 210
Qy 238 QGAELADEMNADIHPSQIEBNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNEPNM 297
Db 211 DAQVFGEEGYS-----SEDAEFYHRQLKLT-QQYTDHCNVNWNVGLNGRGSTYD 261
Qy 298 RWSIFNDYRRYMYITVLDTTAQFSFYDIKRYKDSIGRIGIKTELREIYTTTINFDRLT 357
Db 262 AWVKFNFRREMTLVLDLIVLFPFYDRLYSK-----GVKTELTRDIFTDPI-FSLNT 314
Qy 358 YLEIQPNLATMEYNLRSGLRSLRSLDELIFYTK-----NETYGNRLVGIANRN 406
Db 315 LOEYGPFTLEIENSIRK--HLFDYLOGIEFHLRQPGYSGKDSFNWGSY---VETRP 369
Qy 407 RSTYATTGTBIYGERTPPTTKTLIPFESYKVSIVTDQV--TPTSPPFN--IYFTINQ 462

Db 370 SIGSSKTIITSPFVGDKSTEPVOK--LSPDGQKVY-----RTIANTDVAAMPNGKIYFGVTK 423
Qy 463 IELYLNNSPSNKL-----TYSA-----GGNLNDK---KTTDFQFPVKDKCKPIINPNCL 509
Db 424 VDFSQYDDQKNETSTQTYDSKRNNGHVGAQDSIDQLPPETTD--EPLK----- 470
Qy 510 PSVNSYSHILSQSLFNYSYKIGLALNILYTGALGWTSHSSVNRNNAISDKIITMIPAIG 569
Db 471 ----AYSHQLNYABCFELMODRRGTI--PPFT-----WTHRSVDFFTNIDAEKITQLPVPVKA 520
Qy 570 NSLDTNSKVIIEGPGHTGGLVYLQ-----SQGRLEITCRTPNSTQSYIIRLYATNGAGNT 625
Db 521 YALSSGASIIIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYRVIRYAST----- 575
Qy 626 LPNISLTIPGVIGIPPORLNTFSGTNNYNLQY--GDFGYFOPPPSTVTPLNRNIPF--- 680
Db 576 -TNLRLFV-----QNSNNDFIYIYINKTNWIDDDLTQTDFDLATT---NSNMGFSGD 623
Qy 681 -----IFNRADYSNSILIIDKIEFIPI 702
Db 624 TNELIIGAESFVSNEKIYIDKIEFIPIV 650

Search completed: December 15, 2005, 10:56:39
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:47:44 ; Search time 168 Seconds
(without alignments)
1850.387 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYEIIDSKNLSYP.....FFTNHTKTLNIRATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3623	92.8	694	4	US-10-782-570-4
3	3318	84.9	735	5	US-10-783-417-2
4	1158	29.6	1180	4	US-10-782-141-12
5	1158	29.6	1180	4	US-10-782-096-14
6	1158	29.6	1180	4	US-10-782-570-10
7	1158	29.6	1180	5	US-10-783-417-8
8	1158	29.6	1180	5	US-10-781-979-14
9	901	23.1	1109	3	US-09-756-526A-4
10	901	23.1	1109	4	US-10-345-020-4
11	897	23.0	1109	4	US-10-342-821-4
12	897	23.0	675	4	US-10-782-141-17
13	897	23.0	675	4	US-10-782-096-18
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17	897	23.0	675	5	US-10-926-819-16
18	819	21.0	1136	4	US-10-782-141-13
19	819	21.0	1136	5	US-10-781-979-15
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21	720	18.4	1210	4	US-10-032-717-4
22	720	18.4	1210	4	US-10-414-637-4
23	720	18.4	1210	4	US-10-606-320-4
24	720	18.4	1210	4	US-10-746-914-4
25	712.5	18.2	780	6	US-11-018-615-29
26	712.5	18.2	1169	6	US-11-018-615-25
27	710	18.2	659	4	US-10-614-076-112

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29	710	18.2	659	4	US-10-782-570-9	Sequence 9, Appl
30	710	18.2	659	5	US-10-783-417-7	Sequence 7, Appl
31	709.5	18.2	682	4	US-10-782-096-20	Sequence 20, Appl
32	709.5	18.2	682	4	US-10-782-570-16	Sequence 16, Appl
33	709.5	18.2	682	5	US-10-783-417-14	Sequence 14, Appl
34	709.5	18.2	682	5	US-10-781-979-21	Sequence 21, Appl
35	704	18.0	652	4	US-10-232-665-4	Sequence 4, Appl
36	704	18.0	652	4	US-10-614-076-110	Sequence 110, App
37	703	18.0	1206	4	US-10-032-717-2	Sequence 2, Appl
38	703	18.0	1206	4	US-10-414-637-2	Sequence 2, Appl
39	703	18.0	1206	4	US-10-606-320-2	Sequence 2, Appl
40	703	18.0	1206	4	US-10-746-314-2	Sequence 2, Appl
41	697	17.8	652	4	US-10-232-665-6	Sequence 6, Appl
42	695	17.8	652	4	US-10-232-665-2	Sequence 2, Appl
43	695	17.8	652	4	US-10-614-076-4	Sequence 4, Appl
44	695	17.8	652	4	US-10-614-076-10	Sequence 10, Appl
45	695	17.8	652	4	US-10-614-076-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-10-782-570-2

; Sequence 2, Application US/10782570

; Publication No. US20040210965A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274144

; CURRENT APPLICATION NUMBER: US/10782,570

; CURRENT FILING DATE: 2004-02-19

; PRIOR APPLICATION NUMBER: 60/448,812

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 744

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-782-570-2

Query Match 100.0%; Score 3906; DB 4; Length 744;
Best Local Similarity 100.0%; Pred. No. 4.2e-294;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNQNNEYEIIDSKNLSYPNNIDHSRYPTNNPQPLONTNYKWLNNCCGNTQGD	60
Db	1	MNQNNEYEIIDSKNLSYPNNIDHSRYPTNNPQPLONTNYKWLNNCCGNTQGD	60
Qy	61	NFETFASADTAAVSAGTIVSGTLLAGIGGTSISGPIIGAIISFGTLITVFWPAGE	120
Db	61	NFETFASADTAAVSAGTIVSGTLLAGIGGTSISGPIIGAIISFGTLITVFWPAGE	120
Qy	121	QDKTVTQTFKMGIFVDDTPTLTSIKQLQTLGEGFRQILQSYNTALDDWRKRLQAPG	180
Db	121	QDKTVTQTFKMGIFVDDTPTLTSIKQLQTLGEGFRQILQSYNTALDDWRKRLQAPG	180
Qy	181	LPSSALQQALTKIRFENVHNDPFIETPCFQLETYKTLPIYQAANFHLNLOQA	240
Db	181	LPSSALQQALTKIRFENVHNDPFIETPCFQLETYKTLPIYQAANFHLNLOQA	240
Qy	241	ELADENWADIHPSQIEPNAGTDDYYKLLKENIPKYSNYCANTYREGINKLRNPNMWS	300
Db	241	ELADENWADIHPSQIEPNAGTDDYYKLLKENIPKYSNYCANTYREGINKLRNPNMWS	300
Qy	301	IFNDYRRYMTITVLDITTAQFSFYDIKRYKDSIGRIGGIKTBLTREIYTTINFDRLTYLE	360

Db 301 IFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELTRREIYTTINFDRLTYLE 360
Qy 361 IQPNLAIMEYNLTRSGLRFLSFDELIFPYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420
Db 361 IQPNLAIMEYNLTRSGLRFLSFDELIFPYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420
Qy 421 ERTGPPPTTKLIPPEYSKVSVITDROVTPTPPPNIIYFTINOIELYLNNSPSNKLTVSAG 480
Db 421 ERTGPPPTTKLIPPEYSKVSVITDROVTPTPPPNIIYFTINOIELYLNNSPSNKLTVSAG 480
Qy 481 GNLNDKKTTFDQFPVKKCKPIINPNCPLSYNSYSHILSQPSLFNYSYKIGLALNIIYLT 540
Db 481 GNLNDKKTTFDQFPVKKCKPIINPNCPLSYNSYSHILSQPSLFNYSYKIGLALNIIYLT 540
Qy 541 GALGWTSSVNRNNAISDKIITMIPAIKGNSLDTNSKVIEGPGHTGGLVYLOSQRLEI 600
Db 541 GALGWTSSVNRNNAISDKIITMIPAIKGNSLDTNSKVIEGPGHTGGLVYLOSQRLEI 600
Qy 601 TCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSGTNNIYQYGD 660
Db 601 TCRTPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSGTNNIYQYGD 660
Qy 661 FGYPQPPSTVTLPLNRNIPFENRADVSNLSIIIDKIEFIPITSSVRQNRKQKLETIQT 720
Db 661 FGYPQPPSTVTLPLNRNIPFENRADVSNLSIIIDKIEFIPITSSVRQNRKQKLETIQT 720
Qy 721 KINTFTNHTKNTLINIEATNYDID 744
Db 721 KINTFTNHTKNTLINIEATNYDID 744

RESULT 2

US-10-782-570-4

; Sequence 4, Application US/10782570

; Publication No. US20040210965A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Kozziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274146

; CURRENT APPLICATION NUMBER: US/10/782,570

; CURRENT FILING DATE: 2004-02-19

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 694

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-782-570-4

Query Match 92.8%; Score 3623; DB 4; Length 694;

Best Local Similarity 100.0%; Pred. No. 3.6e-272;

Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 MCOQNTQYGNFETFASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGT 110
Db 1 MCOQNTQYGNFETFASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGT 60
Qy 111 LITVFWPAGEQDKVTWTFQIKMGEIFVDTELTESIKQLKLTLEGFRQLIQSYNTALDDW 170
Db 61 LITVFWPAGEQDKVTWTFQIKMGEIFVDTELTESIKQLKLTLEGFRQLIQSYNTALDDW 120
Qy 171 RKLKRLQAPGLPSSALQQAALTILKIRFENVHNDFREIPGQLEYTKTLLPIYQAAN 230
Db 121 RKLKRLQAPGLPSSALQQAALTILKIRFENVHNDFREIPGQLEYTKTLLPIYQAAN 180

Qy 231 FHLNLQQAELADEWNADIHFSQIEPNAGTSDDDYYKLLKENIPKYSNYCANTYREGLNK 290
Db 181 FHLNLQQAELADEWNADIHFSQIEPNAGTSDDDYYKLLKENIPKYSNYCANTYREGLNK 240
Qy 291 LRNEPNMRWSIFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELTRREIYTTT 350
Db 241 LRNEPNMRWSIFNDYRRYMTITVLDTIAQSFVDIKRYKDSIGRIGGKTELTRREIYTTT 300
Qy 351 INFDRLLTYLEIQPNLAIMEYNLTRSGLRFLSFDELIFPYTKNETYGNRLVGIANRNRSTY 410
Db 301 INFDRLLTYLEIQPNLAIMEYNLTRSGLRFLSFDELIFPYTKNETYGNRLVGIANRNRSTY 360
Qy 411 ATTGTETIYIGERTGPPPTTKLIPPEYSKVSVITDROVTPTPPPNIIYFTINOIELYLNNS 470
Db 361 ATTGTETIYIGERTGPPPTTKLIPPEYSKVSVITDROVTPTPPPNIIYFTINOIELYLNNS 420
Qy 471 PSNKLTYSAGGNSLNDKKTTFDQFPVKKCKPIINPNCPLSYNSYSHILSQPSLFNYSYK 530
Db 421 PSNKLTYSAGGNSLNDKKTTFDQFPVKKCKPIINPNCPLSYNSYSHILSQPSLFNYSYK 480
Qy 531 IGLALNIIYTGALGWTSSVNRNNAISDKIITMIPAIKGNSLDTNSKVIEGPGHTGGLV 590
Db 481 IGLALNIIYTGALGWTSSVNRNNAISDKIITMIPAIKGNSLDTNSKVIEGPGHTGGLV 540
Qy 591 YLOSQRLEICTRPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSG 650
Db 541 YLOSQRLEICTRPNSTQSYIRLRVATNGAGNTLPNISLTIPGVIGIPPORLNNTFSG 600
Qy 651 TYNNLQYGDGFGYFQPPSTVTLPLNRNIPFENRADVSNLSIIIDKIEFIPITSSVRQNR 710
Db 601 TYNNLQYGDGFGYFQPPSTVTLPLNRNIPFENRADVSNLSIIIDKIEFIPITSSVRQNR 660
Qy 711 EKQKLETIQTKINTFTNHTKNTLINIEATNYDID 744
Db 661 EKQKLETIQTKINTFTNHTKNTLINIEATNYDID 694

RESULT 3

US-10-783-417-2

; Sequence 2, Application US/10783417

; Publication No. US20040216186A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Kozziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and

; FILE REFERENCE: 045600/274146

; CURRENT APPLICATION NUMBER: US/10/783,417

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,806

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 735

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-783-417-2

Query Match 84.9%; Score 3318; DB 5; Length 735;

Best Local Similarity 87.1%; Pred. No. 1.9e-248;

Matches 639; Conservative 31; Mismatches 60; Indels 4; Gaps 3;

Qy 1 MNQNN-NNEYEIIDSKNLSYPSNRNIDHSRYPTNNPQLQNTNYKEWLNMCQNTQYG 59
Db 1 MNQNNNNEYEIIDSHTSPYFFNRNSDSRYPTNNPQLQNTNYKEWLNMCQNTQYG 60
Qy 60 DNFETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLLITVFWPAG 119
Db 61 DNFETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLLITVFWPAG 120

Qy 120 EQDVTWTFQIMGEIFVDTPLTBSIKQLKQLTLEGFRQILQSYNTALDWRKLRLOAP 179
 Db 121 EQDVTWTFQIMGEIFVDTPLTBSIKQLKQLTLEGFRQILQSYNTALDWRKLRLOAP 180
 Qy 180 GLPSSALQQAALTLKIRFENVHNDPFIREFIPGFOLEYTKTLLPIYAQAANFHLNLLQOG 239
 Db 181 GLPSSALQQAALTLKIRFENVHNDPFIREFIPGFOLEYTKTLLPIYAQAANFHLNLLQOG 240
 Qy 240 AELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNRW 299
 Db 241 AELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNRW 300
 Qy 300 SIFNDYRYMTITVLDITIAQSFYDIKRYKDSIG--RIGGIKTELTRIETIYTFEINFDRLT 357
 Db 301 SIFNDYRYMTITVLDITIAQSFYDIKRYKDSIG--RIGGIKTELTRIETIYTFEINFDRLT 360
 Qy 358 YLEIQPNLAMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYATTGTEI 417
 Db 361 QLRVQPNLAMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYATTGTEI 420
 Qy 418 IYGBRTGPTTKTLPFESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSPSNKITY 477
 Db 421 LYGBRTGPTTKTLPFESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSPSNKITY 479
 Qy 478 SAGNLNDKKTDFQPPVKCKPIINPNCPLSYNSYSHILSQFSLFNYSYKIGLALNI 537
 Db 480 SAGNLNDKKTDFQPPVKCKPIINPNCPLSYNSYSHILSQFSLFNYSYKIGLALNI 539
 Qy 538 LYTGALGWTSSVNRNNAISDKIITMIPAKGNLSDTNSKVIIEGPGTGGNLYVLOQGR 597
 Db 540 LDVTGLGWTSSVNRNNAISDKIITMIPAKGNLSDTNSKVIIEGPGTGGNLYVLOQGR 599
 Qy 598 LEITCRPNSTQSYIRLRVATNGAGNTLPNISITIPGVIPIPPORLNTFSGTNYNNLQ 657
 Db 600 LEITCRPNSTQSYIRLRVATNGAGNTLPNISITIPGVIPIPPORLNTFSGTNYNNLQ 659
 Qy 658 YGDFGYQFSTVTLPLNRNIPFIPNRADVSNLSIILDKIEFIPITSSVRQNRKQKLET 717
 Db 660 YGDFGYQFSTVTLPLNRNIPFIPNRADVSNLSIILDKIEFIPITSSVRQNRKQKLET 719
 Qy 718 IQTKINTFFTNHTK 731
 Db 720 IQTKINTFFTNHTK 733

RESULT 4

US-10-782-141-12
 ; Sequence 12, Application US/10782141
 ; Publication No. US20040197917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carozzi, Nadine
 ; APPLICANT: Hargiss, Tracy
 ; APPLICANT: Koziel, Michael G.
 ; APPLICANT: Duck, Nicholas B.
 ; APPLICANT: Carr, Brian
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
 ; FILE REFERENCE: 045600/274143
 ; CURRENT APPLICATION NUMBER: US/10782,141
 ; CURRENT FILING DATE: 2004-02-20
 ; PRIOR APPLICATION NUMBER: 60/448,632
 ; PRIOR FILING DATE: 2003-02-20
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 1180
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis
 US-10-782-141-12

Query Match 29.6%; Score 1158; DB 4; Length 1180;
 Best Local Similarity 37.3%; Pred. No. 2e-80;

Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;
 Qy 5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNNPNQPLQNTNYKEWLNMCQGTQYGDNF 62
 Db 6 NKNEYETLNASQKKNLSNN-----YTRYPIENSFKQLQSTNYKDLNMCQONQYGGDF 61
 Qy 63 ETPASADTAAVSAGTIVSGTLGAGIGLTSISOPIGIIGAIISFGTLITVFPAGBQD 122
 Db 62 ETFIDS---GELSAITTVGTVLTGFGFTT---PLGL---ALIGFGTLPVLPFAQDQS 111
 Qy 123 KTVWTFQIMGEIFVDTPLTBSIKQLKQLTLEGFRQILQSYNTALDWRKLRLOAPGLP 182
 Db 112 NT--WSDFIOTKNIKKEIASTYISNANKILNRSFVISTIHNLKWE-----NNNPQ 165
 Qy 183 PSSALQQAALTLKIRFENVHNDPFIREFIP--GFQLEYTKTLLPIYAQAANFHLNLLQOG 240
 Db 166 NTQDVRTQIQLVHVHFQNVIPELVNSCPPNPSDCDYNNILVSSYAQAANLHVLNQA 225
 Qy 241 ELADEWNADHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLREPNR 295
 Db 226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTAKAIEDYTNVCTVYTKGGLNLIKTPDPSNLD 284
 Qy 296 -NNEWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGGIKTELTRIETIYTFEINF 354
 Db 285 GNINWNTYTRYMTTAVLDLVALFPNDVGKPI-----GVQSELTREIYQV-LNFE 337
 Qy 355 RLTYLEIQPNLAMEYNLTSGRLRFLDELIFETKNETYGNRLVGIANRSTYA--- 411
 Db 338 ESPKYY--DFQVQEDSLTRP-HLFTWLDLSLNFYEKAQTTPNPP-TSHYMMFHYTLDN 393
 Qy 412 TTGTETIYGBRTGPTTKTLPFESYKVSIVTDQVTPPTSPFPNIYFTINOIELYLNNSP 471
 Db 394 ISQSSVFGNHNVTDLKSL--GLATNIYIFLLNVI SLDNKLYNNDYNNISQMDFFITNGT 451
 Qy 472 ---SNKLTYSAGNLNDKKTDFQPPVKCKPIINPNCPLSYNSYSHILSQFSLFN 527
 Db 452 RLLEKELT-AGSQITTYDVNKNIFGLFILKRRNQGNPTLFFTYDNTSHILSFKLSJIP 510
 Qy 528 -SYKIGLALNLTGALGWTSSVNRNNAISDKIITMIPAKGNLSDTNSKVIIEGPGHTG 586
 Db 511 ATYK----TQVYTF--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQVPGHTG 563
 Qy 587 GNLVLOSGRLBITCTPNSTQSYIRLRVATNGAGNTLPNISITIPGVIPIPPORLNN 646
 Db 564 GDLI--DFKDFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
 Qy 647 TEGTNYNNLQYDGYFGYFQFSTVTLPLNRNIPFIPNRADV-SNSIILDKIEFIPITSS 705
 Db 621 TFGTDTYNLKXDFQYLFESNEVKFAPNQNISLVFNRSVDYNTNTVTLIDKIEFLPITRS 680
 Qy 706 VRQNRKQKLETIQTKTNTFTTHTKNTLNIETATNYDID 744
 Db 681 IREDREKQKLETVQIINTFYANPKNTLOSELTDYDID 719

RESULT 5

US-10-782-096-14
 ; Sequence 14, Application US/10782096
 ; Publication No. US20040210964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carozzi, Nadine
 ; APPLICANT: Hargiss, Tracy
 ; APPLICANT: Koziel, Michael G.
 ; APPLICANT: Duck, Nicholas B.
 ; APPLICANT: Carr, Brian
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
 ; FILE REFERENCE: 045600/274148
 ; CURRENT APPLICATION NUMBER: US/10782,096
 ; CURRENT FILING DATE: 2004-02-19
 ; PRIOR APPLICATION NUMBER: 60/448,633
 ; PRIOR FILING DATE: 2003-02-20
 ; NUMBER OF SEQ ID NOS: 23

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-14

Query Match      29.6%; Score 1158; DB 4; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

QY 5 NNNEYEIDS--KNLSYSPNRNIDHSRYPTNNPNQPLQNTNYKWLNMCOGNTQYGDNF 62
DB 6 NKNEYETLNASOKKLINNN---YTRYPIENSPKQLQSTNYKDWLNMCQOQQYGGDF 61
QY 63 ETFSADTTAAVSAGTIIVSGTLLAGIGLTSISGPIGIGALIIISFGTLITVFWPAGEQD 122
DB 62 ETFIDS---GELSAYTIIVGTVLTGFGFTT---PLGL---ALIGFTLIPVLFPADQDS 111
QY 123 KTWVTOFIMGEIFVDPTLPTESIKQLKQTLGFRQLOISYNTALDDWRKLRLOAPGLP 182
DB 112 NT-WSDFITQTKNIKKETASTYISNANKILNRSFNVISTYHNHLKTWE-----NNPNPQ 165
QY 183 PSSALQQAALTLKIRFENVHNDPIREIP--GFOLEYTKTLPIYAQAANFHLNLQOGA 240
DB 166 NTQDVRTQIQLVHYHFQNVIPELVNSCPPNPSDCDYNYILVLSYAQAANLHLTVLNQAV 225
QY 241 ELADENWADIHPQIEPNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
DB 226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCTVYTKKGLNLKTTTPDSNLD 284
QY 296 -NMRWSIFNDYRYMTITVLDITAFQSFYDIKRYKDSIGRIGIKTELREIYTTTINFD 354
DB 285 GNNINWNTYRTKMTAVLDLVALFPNVDVGKPI-----GVQSELREIYQV-LNFE 337
QY 355 RLTYLEIQPNLAIMEYNLTSGRLPFLDELIFYTKNETYGNRLVGIANRSTYA---411
DB 338 ESPYKYV--DFQYQEDSLTRP-HLFTWLDLSLNFYEKAQTTNNPF-TSHYNMFTLND 393
QY 412 TTGTETIIGERTGPTTKTILPFESYKVSIVTDROVTPTPSPFNIFTINQIELYLNNSP 471
DB 394 ISQKSSVFGNHNVDKLSL--GLATNIYIFLLNVLSDNKYLDYNNISKMDFFITNGT 451
QY 472 ---SNKLTYSAGNLSNDKKTDFQFPVKCKPCKPIPNPNCPLPSYNSYSHILSQFSLFNY- 527
DB 452 RLLEKELT-AGSQIITYDVNKNIFGLPKRRENGQNPFLFPTYDNYSHILSFIKLSLP 510
QY 528 -SVKIGLALNLYTGALGHTSSVNRNNAISDKIITMIPAIGNSLDTNSKVIEGPGHTG 596
DB 511 ATYK-----TQVYTFE--WTHSSVDPKNTIYTHLTQIPAVKANSLGTSKVVQGPHTG 563
QY 587 GNLVYLQSQGRLEITCRTPNSTQSYIRLYRYATNGAGNTLPNISLTIPGVIGIPQRLNN 646
DB 564 GDLI--DFKDHFKITCQHSNFOQSIFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
QY 647 TFSGTNNYLQYDGFQFPSTVTLPLNRNIPFNRAADV-SNSILIIDKIEFPIITS 705
DB 621 TFSGTYTNLYKDYQFYLEFSNEVKAPNQISLVFNRSDVYNTTNTVLIDKIEFLPIITS 680
QY 706 VRQNEKQKLETIQTINTFTTNNHTKNTLINEATNYDID 744
DB 681 IREDREKQKLETVQOIINTFYANPIKNTLQSELTDYDID 719

RESULT 6
US-10-782-570-10
; Sequence 10, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
```

```
RESULT 7
US-10-783-417-8
; Sequence 8, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274146
; CURRENT FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-8

Query Match      29.6%; Score 1158; DB 5; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy      5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNNPNQPLONTNYKEWLNMCQNTQYGDNF 62
Db      6 NNNEYETLNASQKLNLSNN---YTRYPIENSFKQLQSTNYKDWLNMCQNOQYGGDF 61

Qy      63 ETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIAISFGTLITVFWPAGEQD 122
Db      62 ETFIDS---GELSAYTIWGVLTGFGFTT---PLGL---ALIGFGTLIPVLPFAQDQS 111

Qy      123 KTVMTQFIKGEIFVDPTLPTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQAQCLP 182
Db      112 NT-WSDFITQTKNIKKKIASTYISNANKILNRSFNVISTYVHNLKTWE-----NNPNPQ 165

Qy      183 PSSALQQAALTUKIRFENVHDFIREP--GFQLETYKTLTLLPIYAQAANPHNLQOGA 240
Db      166 NTQDVRTQIQLVHVFHFQNVIPELVNSCPNPSPDCDYNNILVSSYAQAANLHLTVLNQAV 225

Qy      241 ELADEWNADIHPSOIEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTAKAIEDYTNVCTVYKGLNLKTKTPDSNLD 284

Qy      296 -NMRWSIFNDYRYMTITVLTIAQFSFYDIKRYKDSIGRIGGKTELTRIEYTFEINF 354
Db      285 GNINWNTYNTYRTKMTTAVLDLVALFPNYDVGVKYP-----GVQSELTRIEYQV-LNFE 337

Qy      355 RLTYLETOPNLAIMYENLRTSGLRFLFDELIPYTKNETYGNRLVGIANRRTYA---411
Db      338 ESPKYV--DFQVQEDSLTRRP-HLFTWLSLNFYEKAQTTPNNFF-TSHYNMHYTLDN 393

Qy      412 TTGTEIYIGERTGPTTKTLIPESYKVSIVTDQVTPSPFPNIYFTINOIELYLNNSP 471
Db      394 ISQKSSVFGNHNVTDLKSL--GLATNIYIFLLNVLSDNKYLDYNNISKQDFFITNGT 451

Qy      472 ---SNKLTYSAGGNLSNDKKTTFQFPVKQDCKPIINPCLPSYNSYSHILSQSLFNY-527
Db      452 RLLEKELT-AGSGQITVDVKNKIFGLPILKRENGQNPFTPTTYDNYSHILSPFKLSIP 510

Qy      528 -SYKIGALNLTTCALGWTSHSSVNRNNAISDKIITMIPAIGNSLDTNSKIVSGPGHTG 586
Db      511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQTPAVKANSLSGTASKVVGPGHTG 563

Qy      587 GNLVYLOSQGRLELTCRTPNSTQSYVILRYVATGAGNTLPNISLTIPGVIGIPQRLNN 646
Db      564 GDLI--DFKDHFKITCOHNSFQQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620

RESULT 8
US-10-781-979-14
; Sequence 14, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-14

Query Match      29.6%; Score 1158; DB 5; Length 1180;
Best Local Similarity 37.3%; Pred. No. 2e-80;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

Qy      5 NNNEYEIDS--KNLSYPSNRNIDHSRYPTNNPNQPLONTNYKEWLNMCQNTQYGDNF 62
Db      6 NNNEYETLNASQKLNLSNN---YTRYPIENSFKQLQSTNYKDWLNMCQNOQYGGDF 61

Qy      63 ETPASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIAISFGTLITVFWPAGEQD 122
Db      62 ETFIDS---GELSAYTIWGVLTGFGFTT---PLGL---ALIGFGTLIPVLPFAQDQS 111

Qy      123 KTVMTQFIKGEIFVDPTLPTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQAQCLP 182
Db      112 NT-WSDFITQTKNIKKKIASTYISNANKILNRSFNVISTYVHNLKTWE-----NNPNPQ 165

Qy      183 PSSALQQAALTUKIRFENVHDFIREP--GFQLETYKTLTLLPIYAQAANPHNLQOGA 240
Db      166 NTQDVRTQIQLVHVFHFQNVIPELVNSCPNPSPDCDYNNILVSSYAQAANLHLTVLNQAV 225

Qy      241 ELADEWNADIHPSOIEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNEP-----295
Db      226 KFEAYLKNRQFDYLEP-LPTAIDYYPVLTAKAIEDYTNVCTVYKGLNLKTKTPDSNLD 284

Qy      296 -NMRWSIFNDYRYMTITVLTIAQFSFYDIKRYKDSIGRIGGKTELTRIEYTFEINF 354
Db      285 GNINWNTYNTYRTKMTTAVLDLVALFPNYDVGVKYP-----GVQSELTRIEYQV-LNFE 337

Qy      355 RLTYLETOPNLAIMYENLRTSGLRFLFDELIPYTKNETYGNRLVGIANRRTYA---411
Db      338 ESPKYV--DFQVQEDSLTRRP-HLFTWLSLNFYEKAQTTPNNFF-TSHYNMHYTLDN 393

Qy      412 TTGTEIYIGERTGPTTKTLIPESYKVSIVTDQVTPSPFPNIYFTINOIELYLNNSP 471
Db      394 ISQKSSVFGNHNVTDLKSL--GLATNIYIFLLNVLSDNKYLDYNNISKQDFFITNGT 451

Qy      472 ---SNKLTYSAGGNLSNDKKTTFQFPVKQDCKPIINPCLPSYNSYSHILSQSLFNY-527
Db      452 RLLEKELT-AGSGQITVDVKNKIFGLPILKRENGQNPFTPTTYDNYSHILSPFKLSIP 510
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QY 528 -SYKIGLALNLYTGA LGWTHSSVNRNNAISKIITMIPAIKGNSLDTNSKVIEGPGHTG 586
Db 511 ATYK-----TQVYFA--WTHSSVDPKNTIYTHLTQIPAVKANS LGTAS KVVQGPHTG 563
QY 587 GNLVYLOSQRLEITCRTPNSTQSYIRLRYATNGAGNTLPNLSTIPGVIGIPPORLNN 646
Db 564 GDLI--DFKDHFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
QY 647 TFGSTNNNLYQDGFYQFPSTVTLPLNRNIPFIFNRADV-SNSILIIDKIEFIPITSS 705
Db 621 TFGSTDTNLYKDFQYLEFSEVKEFAPNQNISLVFNRSDVYNTTVIDKIEBFLPITRS 680
QY 706 VRQNRQKLETTCTKINTFTNHTKNTLNIEATNYDID 744
Db 681 IREDRQKLETVQIINTFIYAPIKNTLOSELTDYDID 719

RESULT 9
US-09-756-526A-4
; Sequence 4, Application US/09756526A
; Patent No. US20020038005A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913A
; CURRENT APPLICATION NUMBER: US/09/756,526A
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 60/175,158
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-756-526A-4

Query Match 23.1%; Score 901; DB 3; Length 1109;
Best Local Similarity 34.2%; Pred. No. 1.6e-60;
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;

QY 67 SADIIVASAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD-KTV 125
Db 28 SSDTVAVVSAGIVVVGTLT---AFASFVNP---GVVLISFGTLAPVLPDPDEEDPKKI 80

QY 126 WTOPKMGEIFVDTPLTESIKQLKLTLEGFRQILQSYNTALDDWRKLKELQAPGLPPSS 185
Db 81 WSQFMKHGEDLLNQITSTAVKEIALAHLNGFKDVLTYTTERAFNDWKR-----NPSA 131

QY 186 ALQQAALTUKIRFENVHNDPIREIPGQLETYKTLPIYAQAANPHNLNLOQGAELADE 245
Db 132 --NTARLVQSORENAHFNFVSNPQLQPTDYDTLLSCYTEAANLHLNLLHGGVQFADQ 188

QY 246 WNADIHPSQIEPNAGTSDDYYKLLKENIPKSYNCANTYREGINKLRNEPNRWSIFNDY 305
Db 189 WNADQHPSPMLKSSGT---YDELLVYIEKYINCYTKVHKGLNHLKSEKIKTDWAINY 245

QY 306 RRYMTITVLTIAQSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRLYLEIQPNL 365
Db 246 RREMTLVLQVATFPFYDIRFP-----RGVELELTREVYTS-----LDHLTRPPG- 292

QY 366 AIMEYNLTRSGLRFLSFDELIFVTKNETYGNRLVGIANRNRSTYATTGTEI-----IYG 420
Db 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTTGNQFTMKNIYG 335

QY 421. ERTGPPPTK-----TLIPESYKVISVTRQVTPTPSPPNIFTTNIQELIYLNNSPSNK 474
Db 336 N-----TNRLSKQIITLLPGE-FWTHLSINRPFQTIAGINKLYSLIQKI---VFTTFKND 386
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QY 475 LTVSAGNLSND---KKTTFDQFPVKCKOCKPIINPNCLPSYNS--YSHILSOFSLFNYSY 529
Db 387 NEYQKNFNVNQNEPQETNY-----PNDYGGSNSQRPKHNLSHPPLIIHKL 433
QY 530 KIGLALNLYTGA LGWTHSSVNRNNAISKIITMIPAIKGNSLDTNSKVIEGPGHTGNNL 589
Db 434 EFAEYFHSIF--ALGWTNHSVNSQNLISESVSTQPLVKAYEV-TNNSVIRGPGFTGGDL 490
QY 590 VYLOSQRLEITCRTPNSTQSYIRLRYATNGAGNTLPNLSTIPGVIGIPPORLNNPTS 649
Db 491 IELRD--KCSIKCKA--SSLKTYAISLFAAANAIAVSDIVGDSGAGVL-----LQPTFS 541
QY 650 GTNNYN-----LOYGDFGYFQFPSTVTLPLNRNIPFIFNRAD--VSNSTILIIDKIEFPI 702
Db 542 RKGNNFTQDNLNYKDFQYHTLLVDIELPESEIHLKREDDYBEGVILLIDKLEFKPI 601
QY 703 TSSVRQNRQKLETTCTKINTFTNHTKNTLNIEATNYDID 744
Db 602 DENY---TNEMNLEKAKKAVNVLFINAT-NALKMDVTDYHID 639

RESULT 10
US-10-345-020-4
; Sequence 4, Application US/10345020
; Publication No. US20030150018A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeny, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zalunin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913B
; CURRENT APPLICATION NUMBER: US/10/345,020
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-345-020-4

Query Match 23.1%; Score 901; DB 4; Length 1109;
Best Local Similarity 34.2%; Pred. No. 1.6e-60;
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;

QY 67 SADIIVASAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD-KTV 125
Db 28 SSDTVAVVSAGIVVVGTLT---AFASFVNP---GVVLISFGTLAPVLPDPDEEDPKKI 80

QY 126 WTOPKMGEIFVDTPLTESIKQLKLTLEGFRQILQSYNTALDDWRKLKELQAPGLPPSS 185
Db 81 WSQFMKHGEDLLNQITSTAVKEIALAHLNGFKDVLTYTTERAFNDWKR-----NPSA 131

QY 186 ALQQAALTUKIRFENVHNDPIREIPGQLETYKTLPIYAQAANPHNLNLOQGAELADE 245
Db 132 --NTARLVQSORENAHFNFVSNPQLQPTDYDTLLSCYTEAANLHLNLLHGGVQFADQ 188

QY 246 WNADIHPSQIEPNAGTSDDYYKLLKENIPKSYNCANTYREGINKLRNEPNRWSIFNDY 305
Db 189 WNADQHPSPMLKSSGT---YDELLVYIEKYINCYTKVHKGLNHLKSEKIKTDWAINY 245

QY 306 RRYMTITVLTIAQSFYDIKRYKDSIGRIGGIKTELTRTYTTEINFDRLYLEIQPNL 365
Db 246 RREMTLVLQVATFPFYDIRFP-----RGVELELTREVYTS-----LDHLTRPPG- 292

QY 366 AIMEYNLTRSGLRFLSFDELIFVTKNETYGNRLVGIANRNRSTYATTGTEI-----IYG 420
Db 293 -----LFTWLSDIELYTESVAEGDYLSGI-----RESKYTTGNQFTMKNIYG 335
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Db 164 --THANAKAVHDLFTTLEPIIDKDMLKNNASYRIPT-----LPAYAQIATWHLNLLKH 216
Qy 239 GAELADSWNADIHPSQIEPNAGTSDYYK--LLKENIPKYSNYCANTYREGNKLNRNEPM 297
Db 217 AATYNIW---LQNGQINPSTFNSSNYQGYLKRKIQEYTDYCIQTYNAGLTWIRNTNA 273
Qy 298 RWSIFNDYRYMTITVLDIAQFSFYDIKRYKDSIGRIGIKTELTRREIYTTTINFDRLT 357
Db 274 TWNNYTYRLEMTLVLDLIAFPNDPEKYP-----GVKSELIREVY--TWNVSDTFR 326
Qy 358 YLEIQPNLAIMEVNLTRSGRLPSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406
Db 327 -----TITELNGLTRNP--TLFTWINGRFTYRNSRDILDPYDFISFTGNQMA----- 373
Qy 407 RSTYATGTETIYGERG---PPTTKTLIPESY-----KVSIVTDQVTPTSFPNIFYT 459
Db 374 -FTHNDNRNIWGAHVHNIISQDTSKVFPFYRNKPIDKVEIVRHE-----YSD 422
Qy 460 INQIELYNNSPNKLTYSAGGNLSNDKTTDFQFPVKCKPIINPNCPLPSYNSYSHIL 519
Db 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKTDSYMIPKQTK-----NEEYGHTL 471
Qy 520 SQSFLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITWIPAIGNSLDTSKVI 579
Db 472 SYIKTDNYIFSV---VRERRVAFSWHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLOSQRLEITCR--TPNSTQSYIIRLYATNGAGNTLNPISLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDFRVFLKNVSRQVQVIRYATNA-----PKTTVFLTGIDT 581
Qy 639 IPPQRLNNTFSGTNN--NLQYGDGFGYFQFPSTV-----TLPLNRNPIPFNRADV 687
Db 582 ISVE-LPSTTSRQNPATDLTYADFGVYTPRTPVNPNTKTFEGEDTLMT-----LYGTPNH 635
Qy 688 SNSIILIDKIEPIPTSSVRQNRKQKLETIQTKINTFTFN 728
Db 636 SYNI-YIDKIEPIPTQSVLDYTEKQNIKTQKIVNDLFPN 675
RESULT 13
US-10-782-096-18
; Sequence 18, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-18
Query Match 23.0%; Score 897; DB 4; Length 675;
Best Local Similarity 33.0%; Pred. No. 1.6e-60;
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;
Qy 5 NNNYEYIIDSKNLSYSPNRNIDHSRYPTNNQPLQNTNYSKELANCOGNTQYGNFET 64
Db 6 NKNYEYIIPNSGFGSKSNR--YSRYPLANKPQPLKNTNTYKDWLNVCQDNQQYGNAGN 63
Qy 65 FASADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGEQDKT 124

Db 64 FASSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLLPIFW-QGSDPAN 114
Qy 125 VMTQIFKGEIIFVDIPLTE---SIKQLKIQTLLEGFRQILQSNTALDDWRKUKRLQAPGL 181
Db 115 VMQDNLNIG---GRPIQIEDKNIINVLTSIVTPIKNQQLDKYQEFKQKEPAR----- 163
Qy 182 PSSALQQAALTLKIRFENVH--DFIREIPGFQLETYKTLALLPIYAAAPHNLNLLQ 238
Db 164 --THANAKAVHDLFTTLEPIIDKDMLKNNASYRIPT-----LPAYAQIATWHLNLLKH 216
Qy 239 GAELADSWNADIHPSQIEPNAGTSDYYK--LLKENIPKYSNYCANTYREGNKLNRNEPM 297
Db 217 AATYNIW---LQNGQINPSTFNSSNYQGYLKRKIQEYTDYCIQTYNAGLTWIRNTNA 273
Qy 298 RWSIFNDYRYMTITVLDIAQFSFYDIKRYKDSIGRIGIKTELTRREIYTTTINFDRLT 357
Db 274 TWNNYTYRLEMTLVLDLIAFPNDPEKYP-----GVKSELIREVY--TWNVSDTFR 326
Qy 358 YLEIQPNLAIMEVNLTRSGRLPSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406
Db 327 -----TITELNGLTRNP--TLFTWINGRFTYRNSRDILDPYDFISFTGNQMA----- 373
Qy 407 RSTYATGTETIYGERG---PPTTKTLIPESY-----KVSIVTDQVTPTSFPNIFYT 459
Db 374 -FTHNDNRNIWGAHVHNIISQDTSKVFPFYRNKPIDKVEIVRHE-----YSD 422
Qy 460 INQIELYNNSPNKLTYSAGGNLSNDKTTDFQFPVKCKPIINPNCPLPSYNSYSHIL 519
Db 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKTDSYMIPKQTK-----NEEYGHTL 471
Qy 520 SQSFLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITWIPAIGNSLDTSKVI 579
Db 472 SYIKTDNYIFSV---VRERRVAFSWHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLOSQRLEITCR--TPNSTQSYIIRLYATNGAGNTLNPISLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDFRVFLKNVSRQVQVIRYATNA-----PKTTVFLTGIDT 581
Qy 639 IPPQRLNNTFSGTNN--NLQYGDGFGYFQFPSTV-----TLPLNRNPIPFNRADV 687
Db 582 ISVE-LPSTTSRQNPATDLTYADFGVYTPRTPVNPNTKTFEGEDTLMT-----LYGTPNH 635
Qy 688 SNSIILIDKIEPIPTSSVRQNRKQKLETIQTKINTFTFN 728
Db 636 SYNI-YIDKIEPIPTQSVLDYTEKQNIKTQKIVNDLFPN 675
RESULT 14
US-10-782-570-14
; Sequence 14, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-14

Query Match 23.0%, Score 897; DB 4; Length 675;
Best Local Similarity 33.0%; Pred. No. 1.6e-60;
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

QY 5 NNNEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLONTNYKWLNMCOQNTQYGDNPET 64
DB 6 NKNEYEFNAPSNGFSKSN--YRYPLANKPNQPLKNTNYKDWLNVCQDNQOQYGNNA 63
QY 65 PASADTTAAVSAGTIVSGTLLAGIGLTSISGPIIGIIGAIISFGTLITVFWPAGEODKT 124
DB 64 FASSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLPIFW-QGSDPAN 114
QY 125 VMTQFIKMGEIFVDTPLE---SIKOLKLTLEGFRQILOSYNTALDDWRKLRLOAPGL 181
DB 115 WQDOLLNIG---GRPIQIEDKNIINVLTSIVTPIKNQLDKYQEFFDKWEPAR----- 163
QY 182 PPSALQOAAALTAKIRFENVHN---DFIREIPGQLETKYKTLPIVAQAANFHLNLLQ 238
DB 164 --THANAKAVHDLFTTLEPIIDKDLMLKKNASVRIPT-----LPAYAQIATWHLNLLKH 216
QY 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGNKLNEPNM 297
DB 217 AATYNIW---LQOQINPSTENSNNYQGLKKEIQEYTDYCIQTYNAGLTWIRWTNA 273
QY 298 RWSIFNDYRYMTITVLDLIAQFSFYDIKRYKDSIGRIGIKTELTREIYTTTEINFDRLT 357
DB 274 TWMYNTYRLMTLVLDLIAIFNPDPKYP-----GVKSELIREVY--TNVNSDTR 326
QY 358 YLEIQPNLAIMEYNLRSGLRFLSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406
DB 327 -----TITLENGLTRNP--TLFTWINGRFPYRNSRDILDPYDIFSGTGNMA----- 373
QY 407 RSTYATTGTBIYIGERTG---PPTTKTLIPESY---KVSIVTDROVTPSPPPNIYFT 459
DB 374 -FTHNDNRNLINGAVHGNIIISQDTSKVFFPYRNKPIDKVEIVRHR-----YSD 422
QY 460 INQIELYNLSPSKLTYSGAGNLSNDKTTDFOPVKCKPIINPCLPSYNSYSHIL 519
DB 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKRTDSYMPIKQTKW-----NBEYGH 471
QY 520 SQFSLFNYSYKIGLALNLYTGALGWTSHSSVNRNNAISDKIITWIPAKGNSLDTNSKVI 579
DB 472 SYIKTDNYIFSV---VRERRRVAFSWTHTSVDQNTIDLONITQIHALKALKVSSDSKIV 528
QY 580 EGPCHTGGNLVYLOSQRLEITCR--TPNSTQSYIRLRYATNGAGNTLPNLSLTIPGVI 638
DB 582 ISVE-LPSTTSRQPNATDLTYADFGYVTPRTVPNKTFEGEDTLLMT-----LYGTPNH 635
QY 688 SNSLIIDKIEFIPITSSVRQNRKQKLETIQTQKINTFTFN 728
DB 636 SYNI-YIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFVN 675

RESULT 15
US-10-783-417-12
; Sequence 12, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806

; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-12

Query Match 23.0%, Score 897; DB 5; Length 675;
Best Local Similarity 33.0%; Pred. No. 1.6e-60;
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

QY 5 NNNEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLONTNYKWLNMCOQNTQYGDNPET 64
DB 6 NKNEYEFNAPSNGFSKSN--YRYPLANKPNQPLKNTNYKDWLNVCQDNQOQYGNNA 63
QY 65 PASADTTAAVSAGTIVSGTLLAGIGLTSISGPIIGIIGAIISFGTLITVFWPAGEODKT 124
DB 64 FASSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLPIFW-QGSDPAN 114
QY 125 VMTQFIKMGEIFVDTPLE---SIKOLKLTLEGFRQILOSYNTALDDWRKLRLOAPGL 181
DB 115 WQDOLLNIG---GRPIQIEDKNIINVLTSIVTPIKNQLDKYQEFFDKWEPAR----- 163
QY 182 PPSALQOAAALTAKIRFENVHN---DFIREIPGQLETKYKTLPIVAQAANFHLNLLQ 238
DB 164 --THANAKAVHDLFTTLEPIIDKDLMLKKNASVRIPT-----LPAYAQIATWHLNLLKH 216
QY 239 GAELADEWNADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGNKLNEPNM 297
DB 217 AATYNIW---LQOQINPSTENSNNYQGLKKEIQEYTDYCIQTYNAGLTWIRWTNA 273
QY 298 RWSIFNDYRYMTITVLDLIAQFSFYDIKRYKDSIGRIGIKTELTREIYTTTEINFDRLT 357
DB 274 TWMYNTYRLMTLVLDLIAIFNPDPKYP-----GVKSELIREVY--TNVNSDTR 326
QY 358 YLEIQPNLAIMEYNLRSGLRFLSFLDELIFYTKN-----ETY-----GNRLVGIANRN 406
DB 327 -----TITLENGLTRNP--TLFTWINGRFPYRNSRDILDPYDIFSGTGNMA----- 373
QY 407 RSTYATTGTBIYIGERTG---PPTTKTLIPESY---KVSIVTDROVTPSPPPNIYFT 459
DB 374 -FTHNDNRNLINGAVHGNIIISQDTSKVFFPYRNKPIDKVEIVRHR-----YSD 422
QY 460 INQIELYNLSPSKLTYSGAGNLSNDKTTDFOPVKCKPIINPCLPSYNSYSHIL 519
DB 423 IYEMIFFSNS--SEVFRYSSNSTIENNYKRTDSYMPIKQTKW-----NBEYGH 471
QY 520 SQFSLFNYSYKIGLALNLYTGALGWTSHSSVNRNNAISDKIITWIPAKGNSLDTNSKVI 579
DB 472 SYIKTDNYIFSV---VRERRRVAFSWTHTSVDQNTIDLONITQIHALKALKVSSDSKIV 528
QY 580 EGPCHTGGNLVYLOSQRLEITCR--TPNSTQSYIRLRYATNGAGNTLPNLSLTIPGVI 638
DB 582 ISVE-LPSTTSRQPNATDLTYADFGYVTPRTVPNKTFEGEDTLLMT-----LYGTPNH 635
QY 688 SNSLIIDKIEFIPITSSVRQNRKQKLETIQTQKINTFTFN 728
DB 636 SYNI-YIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFVN 675

Search completed: December 15, 2005, 10:59:33
Job time : 171 secs

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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:51:09 ; Search time 13 Seconds
(without alignments)
385.437 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYEIIDSKNLSYP.....FFTNHTKNTLNIEATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pdb.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pdb.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pdb.*
- 4: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pdb.*
- 5: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pdb.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pdb.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pdb.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	18.4	1210	7	US-11-058-727-4
2	720	18.4	1210	7	US-11-058-727-4
3	704	18.0	652	7	US-11-108-389-4
4	703	18.0	1206	7	US-11-108-389-2
5	703	18.0	1206	7	US-11-108-389-2
6	697	17.8	652	7	US-11-108-389-2
7	695	17.8	652	7	US-11-108-389-2
8	683.5	17.5	1386	7	US-11-091-643-6
9	683	17.5	653	7	US-11-192-801-8
10	683	17.5	653	7	US-11-192-801-10
11	683	17.5	653	7	US-11-192-801-12
12	683	17.5	653	7	US-11-192-801-14
13	683	17.5	653	7	US-11-192-801-16
14	683	17.5	653	7	US-11-192-801-18
15	683	17.5	653	7	US-11-192-801-20
16	683	17.5	653	7	US-11-192-801-22
17	683	17.5	653	7	US-11-192-801-24
18	683	17.5	653	7	US-11-192-801-37
19	683	17.5	653	7	US-11-192-801-39
20	679	17.4	673	7	US-11-058-727-14
21	679	17.4	673	7	US-11-108-389-14
22	674	17.3	1316	7	US-11-091-643-4
23	669	17.1	675	7	US-11-058-727-74
24	669	17.1	675	7	US-11-058-727-80
25	669	17.1	675	7	US-11-108-389-74

26 669 17.1 675 7 US-11-108-389-80 Sequence 80, Appl
27 668.5 17.1 674 7 US-11-058-727-82 Sequence 82, Appl
28 668.5 17.1 674 7 US-11-108-389-82 Sequence 82, Appl
29 668 17.1 675 7 US-11-058-727-42 Sequence 42, Appl
30 668 17.1 675 7 US-11-058-727-48 Sequence 48, Appl
31 668 17.1 675 7 US-11-108-389-42 Sequence 42, Appl
32 668 17.1 675 7 US-11-108-389-48 Sequence 48, Appl
33 667.5 17.1 674 7 US-11-058-727-50 Sequence 50, Appl
34 667.5 17.1 674 7 US-11-108-389-50 Sequence 50, Appl
35 666 17.1 673 7 US-11-058-727-70 Sequence 70, Appl
36 666 17.1 673 7 US-11-108-389-70 Sequence 70, Appl
37 665 17.0 673 7 US-11-058-727-34 Sequence 34, Appl
38 665 17.0 673 7 US-11-058-727-68 Sequence 68, Appl
39 665 17.0 673 7 US-11-108-389-34 Sequence 34, Appl
40 665 17.0 673 7 US-11-108-389-68 Sequence 68, Appl
41 664.5 17.0 674 7 US-11-058-727-76 Sequence 76, Appl
42 664.5 17.0 674 7 US-11-108-389-76 Sequence 76, Appl
43 664 17.0 673 7 US-11-058-727-22 Sequence 22, Appl
44 664 17.0 673 7 US-11-058-727-64 Sequence 64, Appl
45 664 17.0 673 7 US-11-058-727-66 Sequence 66, Appl

ALIGNMENTS

RESULT 1

US-11-058-727-4

; Sequence 4, Application US/11058727

; Publication No. US20050261483A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Presnall

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; FILE REFERENCE: 35718/287809

; CURRENT APPLICATION NUMBER: US/11/058,727

; PRIOR FILING DATE: 2005-02-15

; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1210

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-058-727-4

Query Match 18.4%; Score 720; DB 7; Length 1210;

Best Local Similarity 27.5%; Pred. No. 2e-46;

Matches 217; Conservative 137; Mismatches 304; Indels 132; Gaps 30;

QY 1 MNQNNNEYEIIDSKNLSYPNNIDHSRYPTNNPQNTNYKSWLNCCQN-TQYG 59

Db 1 MSPNNQNEYEIIDATSTSVSN---DSNRYPPANEPTNALQNDYKDYKMSAGNASEYP 57

QY 60 DNFETFASADTIAAASAGTIVSGTLLAGIGGLTSISGPIGIIIGAIISFGTLITVFWPAG 119

Db 58 GSPEVLVSGQD--AAKAAIDIVGKLLSGLG-----VPFVGPIVSLYQLDILWPSG 107

QY 120 EQDKTWTQIKWGEIFVDTPFTESIKQLKQLTLEGFRQILQSNTALDDWRKLRQAP 179

Db 108 Q--KSQWEIFMEQVEELINQKIAFYARNKALSEGLEGNNGNYQLYLTALKEWKE----- 158

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QY 180 GLPPSALQQAALTALKIRFENVHNDIFREIPGFOLEYTKTLPIYAQAANFHLNLLQOG 239
Db 159 --NPNGS--RALRDVNRFRFELDSLFTQYMPFSRVNFEVFPFLTVYTOAANLHLLLKDA 214
QY 240 AELADEWNADIHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGLNKLANEPMRW 299
Db 215 SIFGEWGW-----SITINNYYDRQMKLTAEYSDHCWKYETGLAKLGTSAKQW 265
QY 300 SIFNDVRRYMTITVLDIAQFSYDIKRYKDSIGRIGGKTELTRYIT--EINFDR 356
Db 266 VDYNQFRREMTLVLDVVALFPNYDRTYPM-----TKAQLTREYTDPLGAVNVSSI 319
QY 357 -TYLETOPNLAIMYENLITRSLRFLSDELIFTKNET-----YGNRLVGIANRSTY 410
Db 320 GSWYDKAPSGVIESSVIRPP-HVFDYITGLTVYTSRSISSARYIRHWAGHOISVHRIF 378
QY 411 ATTGTETIYGERGTPPTTKLIPFESYKV-SIVTDQVTPTSPPFN---IYFTINQIELY 466
Db 379 SDNI IKQMYGTNQNLHSTST-PDFTNYDIYKTLSDKAVLLDIVFPFGYTYIFFGMEVEFP 437
QY 467 LNNSPSNKLYTSAGNLSNDKTTDFQFPVKDCKPII-----NPNCLPSYNS 514
Db 438 MVN-----QLNTRKTLKN-PVSKD---IAGTRDSELELPPETSQPNYES 481
QY 515 YSHILSQFSLFNYSYKIGLALNLYTGA-----LGWTHSSVNRNNAISDKIITMIPAI 567
Db 482 YSHRLCHIT-----SIPATGSTTGLVPVFSWTHRSADLINAVHSDKITQIPVV 529
QY 568 KGNLSL-----DTNSKVIIEGPGHTGNNLVVLSQGR--EITCRTPNSTQSYVIRLYAT 619
Db 530 KVSDLAPSGITGPNNTVWSPGFTGGGIKVIKIRNGVISHMRVKISDINKYSMRIRYAS 589
QY 620 NGAGNTLPNISLTIPGVIGIPQRLNNTFSGTNNYNNLOYDGFQFOPFSTVTLPLNRNIP 679
Db 590 --ANNTFEYINPSEENVKS-HAOKTMNRGEALTYNKFNYATLPPIKFTTTE-----P 638
QY 680 F-----IFNRADVSNLSIILDKIEPIPTSSVRQREKOKLETIOTKINTFFNHTKNTL 734
Db 639 FITLGAIFEADFLGIEAYIDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKQGL 694
QY 735 NIEATNYDID 744
Db 695 RFGVTDYEVN 704
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RESULT 2

```
US-11-108-389-4
; Sequence 4, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 4
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-108-389-4
```

```
Query Match 18.4%; Score 720; DB 7; Length 1210;
Best Local Similarity 27.5%; Pred. No. 2e-46;
Matches 217; Conservative 137; Mismatches 304; Indels 132; Gaps 30;
```

```
QY 1 MNQNNNEYIIDSKNLSYSPSNRNIDHSRYPTYNPNQPLQNTYKWLNMCOGN-TOYG 59
Db 1 MSPNNQNEVEIIDAETPSTSVSN--DSNRYPPANEPTNALQNMWDYKDKLMSAGNASEYP 57
QY 60 DNFEFTASADTTAAVSAAGTIVSGTLAGIGGUTSISGPIGIGAILIISFGTLITVFWPAG 119
Db 58 GSPEVLVSGQD--AAKAAIDIVGKLLSLG-----VPFVGPIVSLYTQILDILWPSG 107
QY 120 EQDKTWTQFIKMGEIFVDTPLTESI KQKLTQLSGFRQILOSNTALDWRKLRLOAP 179
Db 108 Q--KSQWEIFMQVEELINQKIAEYARNKALSELGLGNYYQLYLTALSEWKE----- 158
QY 180 GLPPSALQQAALTALKIRFENVHNDIFREIPGFOLEYTKTLPIYAQAANFHLNLLQOG 239
Db 159 --NPNGS--RALRDVNRFRFELDSLFTQYMPFSRVNFEVFPFLTVYTOAANLHLLLKDA 214
QY 240 AELADEWNADIHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGLNKLANEPMRW 299
Db 215 SIFGEWGW-----SITINNYYDRQMKLTAEYSDHCWKYETGLAKLGTSAKQW 265
QY 300 SIFNDVRRYMTITVLDIAQFSYDIKRYKDSIGRIGGKTELTRYIT--EINFDR 356
Db 266 VDYNQFRREMTLVLDVVALFPNYDRTYPM-----TKAQLTREYTDPLGAVNVSSI 319
QY 357 -TYLEIQNLAIMYENLITRSLRFLSDELIFTKNET-----YGNRLVGIANRSTY 410
Db 320 GSWYDKAPSGVIESSVIRPP-HVFDYITGLTVYTSRSISSARYIRHWAGHOISVHRIF 378
QY 411 ATTGTETIYGERGTPPTTKLIPFESYKV-SIVTDQVTPTSPPFN---IYFTINQIELY 466
Db 379 SDNI IKQMYGTNQNLHSTST-PDFTNYDIYKTLSDKAVLLDIVFPFGYTYIFFGMEVEFP 437
QY 467 LNNSPSNKLYTSAGNLSNDKTTDFQFPVKDCKPII-----NPNCLPSYNS 514
Db 438 MVN-----QLNTRKTLKN-PVSKD---IAGTRDSELELPPETSQPNYES 481
QY 515 YSHILSQFSLFNYSYKIGLALNLYTGA-----LGWTHSSVNRNNAISDKIITMIPAI 567
Db 482 YSHRLCHIT-----SIPATGSTTGLVPVFSWTHRSADLINAVHSDKITQIPVV 529
QY 568 KGNLSL-----DTNSKVIIEGPGHTGNNLVVLSQGR--EITCRTPNSTQSYVIRLYAT 619
Db 530 KVSDLAPSGITGPNNTVWSPGFTGGGIKVIKIRNGVISHMRVKISDINKYSMRIRYAS 589
QY 620 NGAGNTLPNISLTIPGVIGIPQRLNNTFSGTNNYNNLOYDGFQFOPFSTVTLPLNRNIP 679
Db 590 --ANNTFEYINPSEENVKS-HAOKTMNRGEALTYNKFNYATLPPIKFTTTE-----P 638
QY 680 F-----IFNRADVSNLSIILDKIEPIPTSSVRQREKOKLETIOTKINTFFNHTKNTL 734
Db 639 FITLGAIFEADFLGIEAYIDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKQGL 694
QY 735 NIEATNYDID 744
Db 695 RFGVTDYEVN 704
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RESULT 3

```
US-11-192-801-4
; Sequence 4, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
```

;; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;; CURRENT APPLICATION NUMBER: US/11/192,801
;; CURRENT FILING DATE: 2005-07-29
;; PRIOR APPLICATION NUMBER: US/10/232,665
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US/09/377,466
;; PRIOR FILING DATE: 1999-08-19
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 652
;; TYPE: PRT
;; ORGANISM: Bacillus thuringiensis
US-11-192-801-4

Query Match 18.0%; Score 704; DB 7; Length 652;
Best Local Similarity 29.0%; Pred. No. 1.3e-45;
Matches 217; Conservative 116; Mismatches 272; Indels 142; Gaps 32;
QY 1 MNQNNNEYIID-SKNLSVPSNRIHDSRYPTNNPQNPLQNTNYKSWLNMCQ-GNTQY 58
DB 1 MNPNNRSEHDITKVTNSELPTN---HNQVPLADNENSTLEELNYKEFLRMWEDSSTEV 56
QY 59 GDNFETASADTIA-AVSAGTIVSGTLGAGLTSISGPIGIIIGAILISFGTLITVFPW 117
DB 57 LDN-----STVKDAVGTGIVSVGQILGVVG-----VPFAGALTSFYQSPLDTIWP 101
QY 118 AGEOKTVMTOFKWGEIFVDVTPLTESIKQLKQLTLEGFRQILQSYNTALDDWRKLRLQ 177
DB 102 S---DAPFWKAFMAQVEVLDDKLEEVAKSKALAELOQLQNNFEDYVNALNSWKK----- 153
QY 178 APGLPPSSALQQAALTALKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQAANFHLNLLQ 237
DB 154 ---TPLSLRSKRSQDRIRLEFSAESHFRNSMPSFAVSKPEVLPLPYAQAANTHLLLLK 210
QY 238 QGABLADEWADIHPSQIEPNAGTSDYYKLLKENIPKYSNCANTYREGLNKLNRPNM 297
DB 211 DAQVFGGEWGS-----SEDAEFYHRLQKLT-QQYTDHCNVNWNVGLNGLRGSTDYD 261
QY 298 RWSIFNDYRYMTITVLDITQAQSFYDIKRYKDSIGRIGIKTELTRIEYITTEINFDRLT 357
DB 262 AWKFNFRREMTITVLDLIVLPFYDRLYSK-----GVKTELTRIDFTDPI-FSLNT 314
QY 358 YLEIQPNLAIMEYNLTSLGRLSGLFDELIPYTK-----NETYGNRLVGIANRN 406
DB 315 LQEVGPTFLSIENSIRKP--HLPDYLOQIEHTRLQPGYSKDSFNWWSGNY---VETRP 369
QY 407 RSTVATTGTEIIYERTGPTTKTLIPESYKVSIVTDQV--TPTSPFPN--IYFTINQ 462
DB 370 SIGSKTITSPFYGDKSTEPVQK--LSFDGQKVY---RTIANTDVAAPNGKIYFGVTK 423
QY 463 IELYNLNSPNKL---TVSA-----GGNLSDNK---KTDFQFPVKCKOCKPIINPCL 509
DB 424 VDFSQYDQKNETQTYDSKRNNGHVGADSIDLPPEYD---EPELEK----- 470
QY 510 PSYNSYSHILSQSFLFNYSYKIGIALNLTGALGTHSSVNRNNAISDKIITMIPAIG 569
DB 471 ----AYSHQLNYACFLMQDRGTI--PPFT----WTHRSVDFTIDAELKITOLPVKA 520
QY 570 NSLDTNSKVIPEGHTGGLNLYLO-----SQGRLETCRTPNSTQSYIRLYRYANGAGNT 625
DB 521 YALSSGASIIIEGPGTGNLLFLKSSNSTAKFKVTLNSAALLQRYVRIRYAST----- 575
QY 626 LPNLSLITPGVIGTPQBLNNTSGTYNNLOY--GDFGYQFPSTVTLPLNRNIPF--- 680
DB 576 -TNLRLFV-----QNSNNDFTIVYINKTMNIDDLTYQTFDLATT---NSNMGFSGD 623
681 -----IFNRADVNSILLIDKIEPI 702
624 TNELIIGAEFSVSNKIEYIDKIEPIV 650

RESULT 4
US-11-058-727-2
;; Sequence 2, Application US/11058727
;; Publication No. US20050261483A1
;; GENERAL INFORMATION:
;; APPLICANT: Andre R. Abad
;; APPLICANT: Ronald D. Flannagan
;; APPLICANT: Rafael Herrmann
;; APPLICANT: Theodore W. Kahn
;; APPLICANT: Albert L. Lu
;; APPLICANT: Billy Fred McCutchen
;; APPLICANT: James K. Psenail
;; APPLICANT: James F.H. Wong
;; APPLICANT: Cao-Guo Yu
;; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
;; FILE REFERENCE: 35718/287809
;; CURRENT APPLICATION NUMBER: US/11/058,727
;; CURRENT FILING DATE: 2005-02-15
;; PRIOR APPLICATION NUMBER: 60/391,786
;; PRIOR FILING DATE: 2002-06-26
;; PRIOR APPLICATION NUMBER: 60/460,787
;; PRIOR FILING DATE: 2003-04-04
;; PRIOR APPLICATION NUMBER: 10/606,320
;; PRIOR FILING DATE: 2003-06-25
;; NUMBER OF SEQ ID NOS: 134
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 1206
;; TYPE: PRT
;; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match 18.0%; Score 703; DB 7; Length 1206;
Best Local Similarity 27.6%; Pred. No. 3.7e-45;
Matches 218; Conservative 140; Mismatches 235; Indels 138; Gaps 31;
QY 1 MNQNNNEYIIDSKNLSVPSNRIHDSRYPTNNPQNPLQNTNYKSWLNMCQ-GNTQY 59
DB 1 MSPNNQNEYIIDATPSTSVN---DSNRYPFANEPTNALQNDYDKYKMSAGNASEYP 57
QY 60 DNFETASADTIAAASAGTIVSGTLLAGLTSISGPIGIIIGAILISFGTLITVFPWAG 119
DB 58 GSPEVLVSGD--AAKAAIDIVGKLLSGLG-----VPFVGIVSLYQLDILMPSG 107
QY 120 EQOKTVMTOFKWGEIFVDVTPLTESIKQLKQLTLEGFRQILQSYNTALDDWRKLRLQAP 179
DB 108 E--KSQWEIEMQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALKEWEE----- 158
QY 180 GLPPSSALQQAALTALKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQAANFHLNLLQ 239
DB 159 --NPNGS--RALRDVRNRFELDSLFTQYMPSPFVTFVFPFLTVYAMAANLHLLLLKDA 214
QY 240 ABLADEWADIHPSQIEPNAGTSDYYKLLKENIPKYSNCANTYREGLNKLNRPNRW 299
DB 215 SIFGEWGW-----STTNNYDQMKLTAEYSDHCHVKWYETGLAKLKGTSAKQW 265
QY 300 SIFNDYRYMTITVLDITQAQSFYDIKRYKDSIGRIGIKTELTRIEYITTT---EIFDRL 356
DB 266 VDNQFRETMTAVLDVVALLFPNYDTRTYME-----TKAQLTRVYTDPLGAVNVSSI 319
QY 357 -TYLEIQPNLAIMEYNLTSLGRLSGLFDELIPYTKYKTLTLLPIYAQAANFHLNLLQ 412
DB 320 GSWYDKAPSGVIESSVIRPP-HVFDYITGLTVYTSQSSISARVIRHWAGHQISYHRVS 378
QY 413 TGTEI--IYERTGPTTKTLIPESYKVSIVTDQVTPSPFPN---IYFTINQIELY 466
DB 379 RGSNLQMYGTNQNLHSTST-FDFTNYDIYKLSKDAVLLDIVPGYTYIPFGMEVEFF 437
QY 467 LNNSPSNKLTYSAGNLSNDKTTDFQFPVKCKOCKPIINPCL-----PSYNSVSH 517
DB 438 MVN-----QNNTRKTLKYN-PVSKDIIASTROSELELPPETSDQPNYESYSH 484

QY 518 ILSQSLFNYSYKIGLALNLYTG-----ALGWTSSVNRNNAISDKIITMIPAKGN 570
Db 485 RLCHIT-----SIPATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCW 532
QY 571 SLDTNSKVIIEGPGHTGNLV-YLQSQG-----RLEITCRTPNSQSYIRLRY 617
Db 533 DNLFPFVVKVPGHTGDDLQYNRSTGSGVGTFLFLARYGLALE-----KAGKYRVLRY 595
QY 618 ATNGAGNTLNLISITIPGVIGIPQRLANNFTSGTNNYNLQYDGFYQFPFSTVTLPLNRN 677
Db 586 ATDA-----DIVLHVNDAGIQMPKTMNPG-----EDLTSKTFKVADAITTLNLTADSS 633
QY 678 IPFIENRADVSN-----ILIIDKIEPIPTSSVRQNRKOKLETIQTKINTFTNHTKNT 733
Db 634 LALKHNLGEPDNTSLSGIVVVDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKDG 689
QY 734 LNIEATNYDID 744
Db 690 LRPGVTDYEVN 700

RESULT 5

US-11-108-389-2
; Sequence 2, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-108-389-2

Query Match 18.0%; Score 703; DB 7; Length 1206;
Best Local Similarity 27.6%; Pred. No. 3.7e-45;
Matches 218; Conservative 140; Mismatches 295; Indels 138; Gaps 31;

QY 1 MNQNNNEYIIDSKNLSYPSNRNIDHSRYPTNNPNQPLQNTYKRWLNMCQGN-TOYG 59
Db 1 MSPNNQNEYIIDATPSTSVN---DSNRYPPANEPTNALQNMVDYDKLQMSAGNASEYP 57
QY 60 DNFETPASADTIAVSNAGTIVSGTLLAGIGGLTISGPIGIIIGAILISFGTLITVWPAG 119
Db 58 GSPEVLVSGD--AAKAAIDIVGKLLSGLG-----VPFVGPIVSLYTLQILDIWPAG 107
QY 120 EQDKTVMTQIKMGEIFVDVPTLETESIKOLKQLTLEGFRQLQSYNTALDWRKLKQLAP 179
Db 108 E--KSQWEIPEQVEEELINKIAEYARNKALSELGLGNNYQLYLTALAEWEE----- 158
QY 180 GLPSSALQQAALTQKTRFENVNDPIRETPGQLETYKTLTLLPIYAAQANFHLNLQOG 239
Db 159 --NPNGS--RALRDVRNRFBILDSLFTQYMPSPRVNTFVFPFLTVYVAAANLHLLLKDA 214

QY 240 AELADEWNADIHPSQIEPNAGTSDDDYYKLLKENIKPKYSNYCANTYREGINKLNEPMMRW 239
Db 215 SIFGEWGM-----STTINNYYDRQMKLTATAYSDHCWKYBTGLAKLKGTSAKOW 265
QY 300 SIFNDYRRYMTITVLDTTAAQFSFYDIKRYKDSIGRIGGIKTELTRIEIYTT---EINFDR 356
Db 266 VDYNQFERRENTLAVLDVVALFNYDTRTPME-----TKAQLTREVVYTDPLGAVNVSSI 319
QY 357 -TYLIEQPLNAIMEYNLTRSGLRFLFDELIFYTKNETYGN-RLVGIANRNRSTY--AT 412
Db 320 GSWYDKAPSGFVIESSVIRPP-HVFDYITGLTVYITQSRISISSARYIRHWAGHQISYHRVS 378
QY 413 TGTEI--IYGERTGPTTKTLIPPSYKV-SIVTDROVYTPSPFPN--IYFTINQIELY 466
Db 379 RGSNLQOMYGTQNLHSTST-PDFTNYDIYKTLSDKDAVLDDIVYGYTYIFFGMPSEVFF 437
QY 467 LNNSPSKLTYSGAGNLSNDKKTDFQFVKKDKCPINPNCL-----PSYNSYSH 517
Db 438 MVN-----QLANNTRKTLKYN-PVKDIIASTDSELELPPETSDQPNYESYSH 484
QY 518 ILSQSLFNYSYKIGLALNLYTG-----ALGWTSSVNRNNAISDKIITMIPAKGN 570
Db 485 RLCHIT-----SIPATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCW 532
QY 571 SLDTNSKVIIEGPGHTGNLV-YLQSQG-----RLEITCRTPNSQSYIRLRY 617
Db 533 DNLFPFVVKVPGHTGDDLQYNRSTGSGVGTFLFLARYGLALE-----KAGKYRVLRY 595
QY 618 ATNGAGNTLNLISITIPGVIGIPQRLANNFTSGTNNYNLQYDGFYQFPFSTVTLPLNRN 677
Db 586 ATDA-----DIVLHVNDAGIQMPKTMNPG-----EDLTSKTFKVADAITTLNLTADSS 633
QY 678 IPFIENRADVSN-----ILIIDKIEPIPTSSVRQNRKOKLETIQTKINTFTNHTKNT 733
Db 634 LALKHNLGEPDNTSLSGIVVVDRIEFIPVDETY---EAEQDLEAAKAVNALFTN-TKDG 689
QY 734 LNIEATNYDID 744
Db 690 LRPGVTDYEVN 700

RESULT 6

US-11-192-801-6
; Sequence 6, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic or
; OTHER INFORMATION: non-naturally occurring amino acid sequence encoded by SEQ ID NO.1
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(652)
US-11-192-801-6

Query Match 17.8%; Score 697; DB 7; Length 652;
Best Local Similarity 28.4%; Pred. No. 4.3e-45;
Matches 209; Conservative 121; Mismatches 286; Indels 120; Gaps 28;

Qy	1	MNONNNEYEII	DSKVLSYPSNR	NI	DHGRYPY	TNNP	QPLONT	NYKEWL	AMCO	-	QNTQVG	59	
Db	1	MNPNRSEHDTI	---KVTPN	SELQTNH	QYPLAD	NPNS	TLEE	LNKYKE	FLURMT	EDS	TEVL	57	
Qy	60	DNFETFASADTIA	-AVSAGT	TVSGT	LLAGIG	LTSI	SGPIG	IIGAI	IIISFG	LITVFWPA	118		
Db	58	DN-----	STVKD	AVGTGI	SVVGQ	LGVVG	-----	VPPAG	ALT	TSFYQ	FLNTI	WPS	
Qy	119	GEODKTVM	TOPIKMG	EIVD	TPLT	BSIK	QLOT	LEGFR	QILQS	YNTAL	DDWRK	LKRLQA	
Db	103	---DAD	PMKAFMAQ	VEVL	DKKIE	YAKS	KALAE	LQGL	QNNF	EDYV	NALNS	WKK-----	
Qy	179	PGLPPSSAL	QAAATL	KTRF	ENVH	ND	FIRE	IPG	OLETY	KTL	LLLP	PIYAQA	
Db	154	--TPL	SLRSKRSQ	RIR	ELFS	QAESH	FRNS	MP	SAV	KPEVL	FLPYA	QAANTH	
Qy	239	GAE	LADEN	NADI	HSQI	EP	NAGT	SDDY	KYLK	ENIT	PKYS	NYCANY	
Db	212	AQV	FGEENGYS	-----	SEDA	AFYH	ROLKLT	-QOYT	DHC	VNNY	VNG	LGR	
Qy	299	WSI	FNDV	RYMT	IT	VL	DTIA	QFS	FYDI	KRYK	DSIG	RIGI	
Db	263	WVK	NRFR	REMT	IT	VL	DI	VL	FP	PYDI	R	LYSK-----	
Qy	359	LEI	QNL	AI	MEYN	TR	SG	LR	FS	FL	DE	LI	
Db	316	Q	EY	GT	PL	S	I	E	N	S	I	R	KP-----
Qy	408	STY	ATTG	TEI	I	G	B	T	G	P	P	T	K
Db	371	I	G	S	S	K	T	I	S	P	F	G	D
Qy	464	E	L	I	N	N	S	P	S	K	L-----	TYSA-----	
Db	425	D	F	S	Q	Y	D	D	Q	K	N	E	T
Qy	518	I	L	S	Q	F	L	N	Y	K	I	G	L
Db	475	Q	N	T	A	E	C	F	L	M	D	R	G
Qy	578	V	I	E	G	P	G	H	T	G	N	L	V
Db	529	I	I	E	G	P	F	T	G	N	L	V	K
Qy	634	P	G	V	I	G	I	P					

RESULT 7

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RESUMI
US-11-192-801-2
Sequence 2, Application US/11192801
Publication No. US20050273882A1
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 652
TYPE: PRT

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: ORGANISM: Bacillus thuringiensis
US-11-192-801-2

Query Match      17.8%; Score 695; DB 7; Length 652;
Best Local Similarity 28.4%; Pred. No. 6.1e-45;
Matches 209; Conservative 121; Mismatches 286; Indels 120; Gaps 28;

QY 1 MNQNNNEYELIISKULSYSPNRNIDHSRYPRTYNNPQLONTNYKWLNMCO-GNTQYG 59
DB 1 MNPNNRSEHDTI---KVTPNSELQTNNOYPLADNPNSTLEELNYKEFLRMTEDSFVL 57
QY 60 DNPETPASADTIA-AVSGAGTVSGTLLAGGLTSGISPGIGIAGIIISFGTLITVPWA 118
DB 58 DN-----STVKDAVGTGIVSVQILGVVG-----VPPAGALTSTFQSFNLTWPS 102
QY 119 GEQDKTYVTFIKMGEIFVDTPLTESIKQLKLOTLEGFRQILOSYNTALDDWRKLRLQA 178
DB 103 --DADPWAFMAQVEVLIDKKIEYAKSKALAEQLQNNFEDYVNALSWKK-----153
QY 179 PGLPPSALQQAULTKIRFENVNDIFRIPQFQLETYTKLLPIYQAANFHLNLQO 238
DB 154 --TPLSRKRSQDRIRLELFSQAESHFRNMPSPAVSKFVELFPTVQAANTHLLLLKD 211
QY 239 GAELADSNADIHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGINKLRNEPNMR 298
DB 212 AQVGESEWGY-----SEDVAEFVHRQLKT-QQYTDHCWNVNVGUNGURGSYDA 262
QY 299 WSIENDYRRYMTITVLDTIAQFSPYDIKRYKDSIGRIGGIKTELTRIEIYTFEINFRDLY 358
DB 263 WVKENRFRREMTLVLDLIVLFPPYDIRLYSK-----GVKTELTRDIFTDPI-FSLNLT 315
QY 359 LEIQPNLAIMEYNIITRGLBLFSLDELIIFYTK-----NETYGNRLVGCIANNR 407
DB 316 QEYGTFTLSIENSIRKP-HLFDYLOQIEBFHTLQPGYFGKDSFNYSWGNY---VETRPS 370
QY 408 STVATTGTEIYGBRTGPTTKTLIPESYKSVIVTDQV--TPTSPFN--IYFTINQI 463
DB 371 IGSKTITSPYGDKSTEPVQK--LSPDGGQVY-----RTIANTDVAAMPNGKVYLGVTKV 424
QY 464 ELYLNNSPSNKL---TYSA---GGLNSDNKKTDTDFQPVVKCKCKPIINCLPSYNSYSH 517
DB 425 DFSQYDDQKNETSQTYDSKRNGHVSQAQSID-QLPPTTDEPL-----EKAYSH 474
QY 518 ILSQFSLFNYSYKIGLAINILYTCALGWTSHSVNRNNAISDKIITMIPAKGNSLDNTSK 577
DB 475 QLNAYECFLMQDRAGTI--PFFT-----WTRSHVDFFNTIDAEEKITQLPVVVKAYALS SGA 528
QY 578 VIEGPHTGNNLVLO---SQGRLEITCTPNSQSYVIRLRVATNGAGNLTPLNISITI 633
DB 529 IIEGFGTGNLNUFLKSSNSIAFKVLTLSAALLQYRVRIRYAST-----TNLRLFV 582
QY 634 PGVIGIPQRLNNTFSGTNTN-----NLQYGDGFGYFQFPSTVTLPLNRNIPPIFNRA 686
DB 583 -----QNSNDNFLVIYINKTMNKDDLLTYQTFDLATTNSNMGFSGDKNELIIGAESF 634
QY 687 VNSILLIDKIEFTPI 702
DB 635 VSNEKIYIDKIEFTPV 650

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RESULT 8

US-11-091-643-6
; Sequence 6, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

Db 104 --DADPKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFFEDYVNALNSWK-----154

Qy 180 GLPPSSALQQAALTLKIRFENVHDFIREIPGQLETKYKLLPLPIYAQAANFHLNLLQOG 239

Db 155 -TPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTVAQAANTHLLLLKDA 213

Qy 240 AELADEMNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLNEPN 236

Db 214 QVGEENGWY-----SSEDVAEFYRRLQKLTQQTTHCVNWNVGLNGLRGSTY 261

Qy 297 MRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELTRREIYTTIEINFDR 356

Db 262 DAWKFNRRFRREMTLTVLDLIVLFPFYDIRLYSK-----GVKTELTRDIFTDPI-FLLT 314

Qy 357 TYLEIQNLAIMENYLNTRSGRLRFLSPFLDELIFYTK-----NETYGNRLVGIANR 405

Db 315 TLQKYGPTFLSIENSIRKP--HLFDYLGQIEFHTRLPQGYFGKDSFNWYSGNY---VETR 369

Qy 406 NRSTYATTGTEIYGERGTGPTTKTLIPFESYKVSIVTDROV--TPTSPPN--IYFTIN 461

Db 370 PSIGSSKTIITSPYGDKSTEPVOK--LSFDGQKYV----RTIANTDVAAMPNGKVILGVT 423

Qy 462 QIELYLNNSPSNKL---TYSA---GGNLSNDKKTDPFPVKKDCKPIINPNCLPSYNSY 515

Db 424 KVPFSQYDDQKNETSTQTYDSKRNNGHVSAQDSID--QLPPTTDEPL-----EKAY 473

Qy 516 SHILSQFSLFNYKYKIGLAINILYTGALGHTHSSVNRNNAISDKIITMIPAIGNSLDTN 575

Db 474 SHQLNVAECFLMDRRGTI--PFFT-----WTHRSVDFNTIDAETKITQLPVPVKAYALSSG 527

Qy 576 SKVIEGPGHTGGLNVLYQ-----SQGRLEITCRTPNSTQSYIRLRVATNGAGNTLPNISL 631

Db 528 ASIIEGPGFTGGLNLLFLKSSNSIAKFKVTLSAALLQRYVRIRVAST-----TNLRL 581

Qy 632 TIPGVIGIPQRLNNTFSGTNYN-----NLOYGDFGYFPFSTVTLPLNRNPIPFNR 684

Db 582 FV-----QNSNDFLVIYINKTMKDDLTQYTFDLATTNSNMGFSGDKNELIIGAE 633

Qy 685 ADVNSILLIIDKIEFTPI 702

Db 634 SFVSNKIIYIDKIEFTPIV 651

RESULT 12

US-11-192-801-14

; Sequence 14, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801

; PRIOR FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/10/232,665

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US/09/377,466

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 653

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: peptide encoded by SEQ ID NO:

; FEATURE:

; NAME/KEY: PRT

; LOCATION: (1)..(653)

; OTHER INFORMATION: Cry3Bb1 variant v11231

US-11-192-801-14

Query Match 17.5%; Score 683; DB 7; Length 653;

Best Local Similarity 28.0%; Pred. No. 4.9e-44;

Matches 207; Conservative 122; Mismatches 283; Indels 126; Gaps 28;

Qy 2 NONNNNEYEIIISKNLSPSNNRNIHRSRYPTNNPNQPLONTNYKWLNMCO-GNTQYGD 60

Db 3 NPNNRSEHDTI---KVTNSELQTNHNOYPLADNPNTSTLEELNYKEFLRMTEDSSTEVL 59

Qy 61 NPETPASADTIA-AVSAGTIVSGTLLAGLGGLTSISGPIGIIGAIISFGTLITVWPAG 119

Db 60 N-----STVDKAVGTGIVSVQQLGVVG-----VPFAGALTSTFYQSFLNTTWPS- 103

Qy 120 EODKTWTFQIKMGEIFVDTPLTESIKQLQKLTLEGFRQILOSYNTALDDWRKLRLOAP 179

Db 104 --DADPKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFFEDYVNALNSWK-----154

Qy 180 GLPPSSALQQAALTLKIRFENVHDFIREIPGQLETKYKLLPLPIYAQAANFHLNLLQOG 239

Db 155 -TPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTVAQAANTHLLLLKDA 213

Qy 240 AELADEMNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLNEPN 236

Db 214 QVGEENGWY-----SSEDVAEFYRRLQKLTQQTTHCVNWNVGLNGLRGSTY 261

Qy 297 MRWSIFNDYRRYMTITVLDTIAQFSFYDIKRYKDSIGRIGGIKTELTRREIYTTIEINFDR 356

Db 262 DAWKFNRRFRREMTLTVLDLIVLFPFYDIRLYSK-----GVKTELTRDIFTDPI-FLLT 314

Qy 357 TYLEIQNLAIMENYLNTRSGRLRFLSPFLDELIFYTK-----NETYGNRLVGIANR 405

Db 315 TLQKYGPTFLSIENSIRKP--HLFDYLGQIEFHTRLPQGYFGKDSFNWYSGNY---VETR 369

Qy 406 NRSTYATTGTEIYGERGTGPTTKTLIPFESYKVSIVTDROV--TPTSPPN--IYFTIN 461

Db 370 PSIGSSKTIITSPYGDKSTEPVOK--LSFDGQKYV----RTIANTDVAAMPNGKVILGVT 423

Qy 462 QIELYLNNSPSNKL---TYSA---GGNLSNDKKTDPFPVKKDCKPIINPNCLPSYNSY 515

Db 424 KVPFSQYDDQKNETSTQTYDSKRNNGHVSAQDSID--QLPPTTDEPL-----EKAY 473

Qy 516 SHILSQFSLFNYKYKIGLAINILYTGALGHTHSSVNRNNAISDKIITMIPAIGNSLDTN 575

Db 474 SHQLNVAECFLMDRRGTI--PFFT-----WTHRSVDFNTIDAETKITQLPVPVKAYALSSG 527

Qy 576 SKVIEGPGHTGGLNVLYQ-----SQGRLEITCRTPNSTQSYIRLRVATNGAGNTLPNISL 631

Db 528 ASIIEGPGFTGGLNLLFLKSSNSIAKFKVTLSAALLQRYVRIRVAST-----TNLRL 581

Qy 632 TIPGVIGIPQRLNNTFSGTNYN-----NLOYGDFGYFPFSTVTLPLNRNPIPFNR 684

Db 582 FV-----QNSNDFLVIYINKTMKDDLTQYTFDLATTNSNMGFSGDKNELIIGAE 633

Qy 685 ADVNSILLIIDKIEFTPI 702

Db 634 SFVSNKIIYIDKIEFTPIV 651

RESULT 13

US-11-192-801-16

; Sequence 16, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801

; PRIOR FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/10/232,665

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US/09/377,466

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

```

; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: Cry3Bb1 variant v11231
US-11-192-801-16

Query Match      17.5%; Score 683; DB 7; Length 653;
Best Local Similarity 28.0%; Pred. No. 4.9e-44;
Matches 207; Conservative 122; Mismatches 283; Indels 126; Gaps 28;

Qy  2 NONNNEYEIDSKVLSYPSNRNIDHSRYPTNNPQPLQNTYKWLNMCO-QNTQYGD 60
Db  3 NPNRSEHDTI---KVTNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDSSTEVL 59
Qy  61 NFETASADTIA-AVSAGTIVSGTLGAGIGLTSISGPIGIIAGIIISFGTLITVFPAG 119
Db  60 N-----STVKDAVGTSVVGQILGVG-----VFPAGALTSFYQSLNTIWP 103
Qy  120 EQDKVTWQTKMGEIFVDTPLTESIKQLKLTLEGFRQILQSYNTALDWRKLRLOAP 179
Db  104 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFEDYVNALNSWK----- 154
Qy  180 GLPSSALQQAALTAKIRFENVHNDFTREIPGQLETKYKTLPIYAAQANFHLNLQOG 239
Db  155 -TPLSLRKSGQRIRELFSQAESHFNPSFSAVSKFEVLFLPTYAQAANTHLLLLKDA 213
Qy  240 AELADENADHPSQIEPNAGTSD---YVKLLKENIPKYSNVCANTYREGNKLNEPN 296
Db  214 QVGEENG-----SSEDVAEFRRQLKLTQYTDHCVNWNVYVGLNGLRSTY 261
Qy  297 MRWSIFNDYRYRMTITVLDITAOFSFYDIKRYKDSIGRIKIGIKTELREIYTTIEIN 356
Db  262 DAWKFNRRERMTLVLDLIVLPFFYDIRLYSK-----GVKTELTRDIFTDPI-FL 314
Qy  357 TYLEIQNLAIMENYLRSGRLRPSFLDELIFYTK-----NETYGNRLVGIANR 405
Db  315 TLQYGTPLFSIENSIRKP--HLFDYLGQIEFHTRLPGYFGKDSFNWWSGN---VETR 369
Qy  406 NRSTYATTGTEIYGERGTPTTKTLIPESYKSVITDROV--TPTSPFPN--IYFTIN 461
Db  370 PSTGSKTITSPFYGDKSTFVQK--LSFDGQKY-----RTIANTDVAAMPNGKVIL 423
Qy  462 QIELYLNNSPNKL---TYSA---GGNLSNDKKTTFQFPVKDCKPIINPNCPLPSYNS 515
Db  424 KVDFSOYDDQKNETSTQYDSKRNHVSQAQSDID--QLPPTTDEPL-----EKAY 473
Qy  516 SHILSQSLFNYSYKIGLALNLYTGALGTHSVNRNNAISDKIITMIPAIGNSLDTN 575
Db  474 SHQLNYAECFLMQDRRGTI--PFFT---WTHRSVDFPNTIDAEKITQLPVRKAYALS 527
Qy  576 SKVIEGPGHTGGLNVLVQ----SQGLEICRTPNSTQSYVIRLYATNGAGNLTPLNIS 631
Db  528 ASIIEGPGFTGGNLLFLKESNSIAKPKVTLNSAALLQRYVRIRYAST-----TN 581
Qy  632 TIPGVIGIPQRLNNTFSGTNYN-----NLOYGDFGYFQFPSTVTLPLNRNIPFENR 684
Db  582 FV-----QNSNDFLVIIYINKTKDDDLTYQTDFLATTNSNMGFSGDKNELIIGAE 633

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RESULT 14

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US-11-192-801-18
; Sequence 18, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

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; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
US-11-192-801-18

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Query Match      17.5%; Score 683; DB 7; Length 653;
Best Local Similarity 28.0%; Pred. No. 4.9e-44;
Matches 207; Conservative 122; Mismatches 283; Indels 126; Gaps 28;

Qy  2 NONNNEYEIDSKVLSYPSNRNIDHSRYPTNNPQPLQNTYKWLNMCO-QNTQYGD 60
Db  3 NPNRSEHDTI---KVTNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDSSTEVL 59
Qy  61 NFETASADTIA-AVSAGTIVSGTLGAGIGLTSISGPIGIIAGIIISFGTLITVFPAG 119
Db  60 N-----STVKDAVGTSVVGQILGVG-----VFPAGALTSFYQSLNTIWP 103
Qy  120 EQDKVTWQTKMGEIFVDTPLTESIKQLKLTLEGFRQILQSYNTALDWRKLRLOAP 179
Db  104 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQGNFEDYVNALNSWK----- 154
Qy  180 GLPSSALQQAALTAKIRFENVHNDFTREIPGQLETKYKTLPIYAAQANFHLNLQOG 239
Db  155 -TPLSLRKSGQRIRELFSQAESHFNPSFSAVSKFEVLFLPTYAQAANTHLLLLKDA 213
Qy  240 AELADENADHPSQIEPNAGTSD---YVKLLKENIPKYSNVCANTYREGNKLNEPN 296
Db  214 QVGEENG-----SSEDVAEFRRQLKLTQYTDHCVNWNVYVGLNGLRSTY 261
Qy  297 MRWSIFNDYRYRMTITVLDITAOFSFYDIKRYKDSIGRIKIGIKTELREIYTTIEIN 356
Db  262 DAWKFNRRERMTLVLDLIVLPFFYDIRLYSK-----GVKTELTRDIFTDPI-FL 314
Qy  357 TYLEIQNLAIMENYLRSGRLRPSFLDELIFYTK-----NETYGNRLVGIANR 405
Db  315 TLQYGTPLFSIENSIRKP--HLFDYLGQIEFHTRLPGYFGKDSFNWWSGN---VETR 369
Qy  406 NRSTYATTGTEIYGERGTPTTKTLIPESYKSVITDROV--TPTSPFPN--IYFTIN 461
Db  370 PSTGSKTITSPFYGDKSTFVQK--LSFDGQKY-----RTIANTDVAAMPNGKVIL 423
Qy  462 QIELYLNNSPNKL---TYSA---GGNLSNDKKTTFQFPVKDCKPIINPNCPLPSYNS 515
Db  424 KVDFSOYDDQKNETSTQYDSKRNHVSQAQSDID--QLPPTTDEPL-----EKAY 473
Qy  516 SHILSQSLFNYSYKIGLALNLYTGALGTHSVNRNNAISDKIITMIPAIGNSLDTN 575
Db  474 SHQLNYAECFLMQDRRGTI--PFFT---WTHRSVDFPNTIDAEKITQLPVRKAYALS 527
Qy  576 SKVIEGPGHTGGLNVLVQ----SQGLEICRTPNSTQSYVIRLYATNGAGNLTPLNIS 631
Db  528 ASIIEGPGFTGGNLLFLKESNSIAKPKVTLNSAALLQRYVRIRYAST-----TN 581
Qy  632 TIPGVIGIPQRLNNTFSGTNYN-----NLOYGDFGYFQFPSTVTLPLNRNIPFENR 684
Db  582 FV-----QNSNDFLVIIYINKTKDDDLTYQTDFLATTNSNMGFSGDKNELIIGAE 633

```


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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:34:42 ; Search time 189 Seconds
(without alignments)
1729.618 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEVEIIDSKNLSYP.....FFTNHTKNTLNIBATNYDID 744

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004as.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3906	100.0	744	8	ADR89397
2	3623	92.8	694	8	ADR89399
3	3318	84.9	735	8	ADR89395
4	1159	29.7	1180	1	RAP93715
5	1158	29.6	1180	8	ADR89426
6	1157	29.6	1016	1	RAP94035
7	1157	29.6	1180	1	RAP82589
8	1153	29.5	1180	2	AAR14373
9	1153	29.5	1180	2	AAR63078
10	901	23.1	1109	5	RAE26353
11	901	23.1	1109	7	ADF31302
12	901	23.1	1109	7	ADF31307
13	900	23.0	686	2	AAR63079
14	899	23.0	675	2	AAR14374
15	897	23.0	675	8	ADR89431
16	897	23.0	675	9	ADY59866
17	819	21.0	1136	5	AAU76029
18	819	21.0	1136	8	ADR89427
19	819	21.0	1136	9	AEA61391
20	818	20.9	1136	1	RAP93341
21	816	20.9	1136	1	RAP82314
22	791.5	20.3	1169	2	AAW06417
23	772.5	19.8	1095	1	AAP97052
24	755	19.3	1178	1	AAP60051

25	720	18.4	1210	5	AAU99256
26	720	18.4	1210	8	ADL15307
27	720	18.4	1210	9	AEb45609
28	712.5	18.2	780	9	AEA81472
29	712.5	18.2	1169	9	AEA81468
30	710	18.2	651	2	AAW06460
31	710	18.2	651	2	AAW06419
32	710	18.2	659	2	AAAY23213
33	710	18.2	659	8	ADR89424
34	709.5	18.2	682	8	ADR89433
35	704	18.0	652	2	AAAY23211
36	704	18.0	652	3	AAAY70442
37	704	18.0	652	6	ABU09193
38	704	18.0	652	7	ABW01051
39	703	18.0	1206	5	AAU99255
40	703	18.0	1206	8	ADL15305
41	703	18.0	1206	9	AEb45607
42	699	17.9	651	2	RAR33769
43	697	17.8	652	3	AAAY70443
44	697	17.8	652	6	ABU09194
45	697	17.8	652	7	ABW01052

ALIGNMENTS

RESULT 1	
ADR89397	
ID	ADR89397 standard; protein; 744 AA.
XX	
AC	ADR89397;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	AXMI-007.
XX	
KW	delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KW	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
Key	Location/Qualifiers
FF	
FT	Misc-difference 1
XX	/note= "encoded by GTG"
XX	
PN	WO2004074462-A2.
XX	
PD	02-SEP-2004.
XX	
PPF	20-FEB-2004; 2004WO-US005829.
XX	
PR	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.
PR	20-FEB-2003; 2003US-0448797P.
PR	20-FEB-2003; 2003US-0448806P.
PR	20-FEB-2003; 2003US-0448810P.
PR	20-FEB-2003; 2003US-0448812P.
PR	19-FEB-2004; 2004US-00781979.
PR	19-FEB-2004; 2004US-00782020.
PR	19-FEB-2004; 2004US-00782096.
PR	19-FEB-2004; 2004US-00782141.
PR	19-FEB-2004; 2004US-00782570.
PR	19-FEB-2004; 2004US-00783417.
XX	
PA	(ATHE-) ATHENIX CORP.
XX	
PI	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX	
DR	WPI; 2004-635574/61.
DR	N-PSDB; ADR89396.
XX	

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 9; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
 XX endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX Sequence 744 AA;

Query Match	100.0%;	Score 3906;	DB 8;	Length 744;
Best Local Similarity	100.0%;	Pred. No. 1.6e-304;		
Matches 744;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNQNNNEYEIIDS	KNLSYSPNRNIDHSRY	PDYNNPNQPLQNTNYKEWLNMCQNTQYGD 60
DB	1	MNQNNNEYEIIDS	KNLSYSPNRNIDHSRY	PDYNNPNQPLQNTNYKEWLNMCQNTQYGD 60
QY	61	NFETASADTIAV	SAGTIVSGTLLAGIGL	TSISGPIIGIIGAIISFGTLITVFPAGE 120
DB	61	NFETASADTIAV	SAGTIVSGTLLAGIGL	TSISGPIIGIIGAIISFGTLITVFPAGE 120
QY	121	QDKTWTQFKMGE	IFVDTPLTESIKQLQ	TLQLEGFRQILQSYNTALDDMRKRLQAPG 180
DB	121	QDKTWTQFKMGE	IFVDTPLTESIKQLQ	TLQLEGFRQILQSYNTALDDMRKRLQAPG 180
QY	181	LPSSALQQAALT	KLKRFENVHNDFREI	PGFOLEYKTLTLLPIYAQAANFHLNLLQOGA 240
DB	181	LPSSALQQAALT	KLKRFENVHNDFREI	PGFOLEYKTLTLLPIYAQAANFHLNLLQOGA 240
QY	241	ELADEWNADTH	PSQIEPNAGTSDDY	YKLLKENIPKYSNYCANTYREGLNKRNPNRWS 300
DB	241	ELADEWNADTH	PSQIEPNAGTSDDY	YKLLKENIPKYSNYCANTYREGLNKRNPNRWS 300
QY	301	IFNDYRYMTIT	VLDTIAQSFYDIKRY	KDSIGRIGGIKTELTRIIYTTTEINFDRLTYLE 360
DB	301	IFNDYRYMTIT	VLDTIAQSFYDIKRY	KDSIGRIGGIKTELTRIIYTTTEINFDRLTYLE 360
QY	361	IQPNLAIMEY	NLRSGLRSLFSDEL	IFYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420
DB	361	IQPNLAIMEY	NLRSGLRSLFSDEL	IFYTKNETYGNRLVGIANRNRSTVATTGTEIIYG 420
QY	421	ERTGPPTTKL	IPESYKVSIVTDQ	VTPTSPPNIIYFTINQELYNLNSPSNKLTVSAG 480
DB	421	ERTGPPTTKL	IPESYKVSIVTDQ	VTPTSPPNIIYFTINQELYNLNSPSNKLTVSAG 480
QY	481	GNLSNDKKT	TDFFQPVVKDCKP	IINPNCLPSYNSYSHLSQFSLEFNYSYKIGLALNIIYT 540
DB	481	GNLSNDKKT	TDFFQPVVKDCKP	IINPNCLPSYNSYSHLSQFSLEFNYSYKIGLALNIIYT 540
QY	541	GALGWTSSV	NRNNAISDKIITW	IPAKNSLDTNSKVIEGPGHTGGLNVLQSQRLLEI 600
DB	541	GALGWTSSV	NRNNAISDKIITW	IPAKNSLDTNSKVIEGPGHTGGLNVLQSQRLLEI 600
QY	601	TCRTPNSTQ	SYIYLRVATNGAG	NLPIISLTIPGVIGIPQRLNNTFSGTNNYNNIYQGD 660
DB	601	TCRTPNSTQ	SYIYLRVATNGAG	NLPIISLTIPGVIGIPQRLNNTFSGTNNYNNIYQGD 660
QY	661	FGYFQFPST	VTPLPNRNIPFI	FNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720
DB	661	FGYFQFPST	VTPLPNRNIPFI	FNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720

Db	661	FGYFQFPSTVTPLPNRNIPFI	FNRAVDSNLSILIDKIEFIPITSSVRQNRKQKLETIQT 720
QY	721	KINTFFTNTKNTLNIEATNYDID	744
DB	721	KINTFFTNTKNTLNIEATNYDID	744

RESULT 2

ADR89399
 ID ADR89399 standard; protein; 694 AA.

XX ADR89399;

DT 18-NOV-2004 (first entry)

XX AXMI-007 alternative protein.

XX delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.

XX Bacillus thuringiensis.

PN WO200407462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

PR 20-FEB-2003; 2003US-0448633P.

PR 20-FEB-2003; 2003US-0448797P.

PR 20-FEB-2003; 2003US-0448806P.

PR 20-FEB-2003; 2003US-0448810P.

PR 19-FEB-2003; 2003US-0448812P.

PR 19-FEB-2004; 2004US-00781979.

PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.

PR 19-FEB-2004; 2004US-00782141.

PR 19-FEB-2004; 2004US-00782570.

PR 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

DR N-PSDB; ADR89398.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 11; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX Sequence 694 AA;

Query Match		92.8%; Score 3623; DB 8; Length 694;
Best Local Similarity		100.0%; Pred. No. 8e-282;
Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	51	MCQNTQYQDNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAILIISFGT 110
Db	1	MCQNTQYQDNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAILIISFGT 60
Qy	111	LITVFWPAGEODKVTWQTFIKMGEIFVDTPLETESI KQLKLTLEGFRQILQSNTALDDW 170
Db	61	LITVFWPAGEODKVTWQTFIKMGEIFVDTPLETESI KQLKLTLEGFRQILQSNTALDDW 120
Qy	171	RKLKQLQAPGLPPSALQQAALTILKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQAN 230
Db	121	RKLKQLQAPGLPPSALQQAALTILKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQAN 180
Qy	231	PHNLLOQGAELADENADIHPSQIEPNAGTSDDYVYKLLKENIPKYSNYCANTYREGLNK 290
Db	181	PHNLLOQGAELADENADIHPSQIEPNAGTSDDYVYKLLKENIPKYSNYCANTYREGLNK 240
Qy	291	LRNEPNRWSIFNDYRRYMTITVLDTTIAQFSFYDIKRYKDSIGRIGGKTREIYVTE 350
Db	241	LRNEPNRWSIFNDYRRYMTITVLDTTIAQFSFYDIKRYKDSIGRIGGKTREIYVTE 300
Qy	351	INFRLTYLEIQPNLAIMEYNLTRSGLRFLPSFLDELIFYTKNETYGNRLVGIANRSTY 410
Db	301	INFRLTYLEIQPNLAIMEYNLTRSGLRFLPSFLDELIFYTKNETYGNRLVGIANRSTY 360
Qy	411	ATTGTEIYIGERTGPTTKTILIPESYKSVITVDQVTPSPFPNIYFTINOIELYLNN 470
Db	361	ATTGTEIYIGERTGPTTKTILIPESYKSVITVDQVTPSPFPNIYFTINOIELYLNN 420
Qy	471	PSNKLTYSAGNLSNDKTTDFQFPVKCKDCKPIINPNCLPSYNSYSHLSQFSLFNYSYK 530
Db	421	PSNKLTYSAGNLSNDKTTDFQFPVKCKDCKPIINPNCLPSYNSYSHLSQFSLFNYSYK 480
Qy	531	IGLALNLYTGALGWTSSVNRNNAISDKITIMIPAIKGNSLDTSNKGIEGHTGNLV 590
Db	481	IGLALNLYTGALGWTSSVNRNNAISDKITIMIPAIKGNSLDTSNKGIEGHTGNLV 540
Qy	591	YLOSQGLEITCRPNSTQSYIRLYATNGAGNTLPNISITIPGVIGIPQRLNNTFSG 650
Db	541	YLOSQGLEITCRPNSTQSYIRLYATNGAGNTLPNISITIPGVIGIPQRLNNTFSG 600
Qy	651	TNYYNLOQDGYQFPSTVTLPLNRNIPFIFNRADVSNLSILIIDKIEFIPITSSVRQNR 710
Db	601	TNYYNLOQDGYQFPSTVTLPLNRNIPFIFNRADVSNLSILIIDKIEFIPITSSVRQNR 660
Qy	711	EKQKLEITQKINTFFNHTKNTLNIEATNYDID 744
Db	661	EKQKLEITQKINTFFNHTKNTLNIEATNYDID 694
RESULT 3		
ADR89395		
ID	ADR89395	standard; protein; 735 AA.
XX	XX	
AC	AC	ADR89395;
XX	XX	
DT	18-NOV-2004	(first entry)
XX	XX	
DE	AXMI-006.	
XX	XX	
KW	KW	delta-endotoxin; delta-endotoxin associate polypeptide;
KW	KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	KW	lepidoptera; coleoptera; pest; pesticide; resistance;
XX	XX	pesticidal activity.
OS	OS	Bacillus thuringiensis.
XX	XX	
PN	PN	W02004074462-A2.
XX	XX	
PD	PD	02-SEP-2004.

20-FEB-2004; 2004WO-US005829.
20-FEB-2003; 2003US-0448632P.
20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-0448797P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448812P.
20-FEB-2004; 2004US-00781979.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-00782141.
19-FEB-2004; 2004US-00782570.
19-FEB-2004; 2004US-00783417.

(ATHE-) ATHENIX CORP.

Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

WPI; 2004-635574/61.

N-PSDB; ADR89394.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Claim 12; SEQ ID NO 7; 178pp; English.

This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

Sequence 735 AA;

Query Match 84.9%; Score 3318; DB 8; Length 735;
Best Local Similarity 87.1%; Pred. No. 2.9e-257;
Matches 639; Conservative 31; Mismatches 60; Indels 4; Gaps 3;

Qy	1	MNQNN-NNEYEIIIDSKNLSYPNSNRNIDHSRYPVTNNPQNPLQNTNYKEWLNMCQNTQYG 59
Db	1	MNQNN-NNEYEIIIDSKNLSYPNSNRNIDHSRYPVTNNPQNPLQNTNYKEWLNMCQNTQYG 60
Qy	60	DNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAILIISFGTLITVFWPAG 119
Db	61	DNFETPASADTTAAVSAGTIVSGTLLAGIGGLTSISGPIIGIIGAILIISFGTLITVFWPAG 120
Qy	120	EQDKTWTQIKMGEIFVDTPLETESI KQLKLTLEGFRQILQSNTALDDWRKLRLOAP 179
Db	121	EQDKTWTQIKMGEIFVDTPLETESI KQLKLTLEGFRQILQSNTALDDWRKLRLOAP 180
Qy	180	GLPPSSALQQAALTILKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQANFHLNLQOG 239
Db	181	GLPPSSALQQAALTILKIRFENVHNDPIREIPGQLETKYKTLTLLPIYAQANFHLNLQOG 240
Qy	240	AELADEWNADIHPSQIEPNAGTSDDYVYKLLKENIPKYSNYCANTYREGLNKLRNEPNRW 299
Db	241	AELADEWNADIHPSQIEPNAGTSDDYVYKLLKENIPKYSNYCANTYREGLNKLRNEPNRW 300
Qy	300	SIFNDYRRYMTITVLDTTIAQFSFYDIKRYKDSIG--RIGGKTREIYVTEINFRLP 357
Db	301	SIFNDYRRYMTITVLDTTISQFSLYDIKRYRDSIGGIEVKGKIKELTREIYVTEINFRLP 360

pesticidal activity.
 KW OS Bacillus thuringiensis.
 XX XX WO2004074462-A2.
 XX XX 02-SEP-2004.
 XX XX 20-FEB-2004; 2004WO-US005829.
 XX XX 20-FEB-2003; 2003US-0448632P.
 XX XX 20-FEB-2003; 2003US-0448633P.
 XX XX 20-FEB-2003; 2003US-0448797P.
 XX XX 20-FEB-2003; 2003US-0448806P.
 XX XX 20-FEB-2003; 2003US-0448810P.
 XX XX 20-FEB-2003; 2003US-0448812P.
 XX XX 19-FEB-2004; 2004US-00781979.
 XX XX 19-FEB-2004; 2004US-00782020.
 XX XX 19-FEB-2004; 2004US-00782096.
 XX XX 19-FEB-2004; 2004US-00782141.
 XX XX 19-FEB-2004; 2004US-00782570.
 XX XX 19-FEB-2004; 2004US-00783417.
 XX XX (ATHE-) ATHENIX CORP.
 XX XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX XX WPI; 2004-635574/61.
 XX XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX XX Example 6; SEQ ID NO 38; 178pp; English.
 XX XX This sequence represents a delta-endotoxin crystal protein. This protein
 CC was included in the scope of the invention as a comparison to the delta-
 CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
 CC of the invention have alternative start codons, producing more than one
 CC protein from a single open reading frame. The nucleic acid sequences of
 CC the invention are useful in DNA constructs or expression cassettes for
 CC transformation and expression in plants and bacteria. The nucleic acids
 CC and corresponding polypeptides are useful for killing lepidopteran or
 CC coleopteran pests. Compositions containing the delta-endotoxins of the
 CC invention, and methods for their production, are useful for the
 CC production of organisms with pesticide resistance, specifically bacteria
 CC and plants. These organisms are useful for generating altered or improved
 CC delta-endotoxin or delta-endotoxin-associated proteins that have
 CC pesticidal activity, or for detecting the presence of delta-endotoxin or
 CC delta-endotoxin-associated proteins or nucleic acids in products or
 CC organisms.
 XX XX Sequence 1180 AA;
 SQ
 Query Match 29.6%; Score 1158; DB 8; Length 1180;
 Best Local Similarity 37.3%; Pred. No. 2.8e-83;
 Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;
 QY 5 NNNVEYIIDS--KNLSYPSNENIDHSRYPTNNPQLONTNYKEWLNMCQNTQYGDNF 62
 DB 6 NKNYEYTLNLSAQKLNLSNN----YTRYPIENSQKLLQSTNYKDLNMCQNNQYGGDF 61
 QY 63 ETFASADTIAVASAGTIVSGTLGAGLTSISGPIGAIISFGTLITVFWPAGEQD 122
 DB 62 ETFIDS---GELSAITVVGVLGFGFTT---PLGL---ALIGFTGLPLVFPADQDS 111
 QY 123 KTVMTQIKMGEIFVDTPLETESIKQLKQTLLEGFRQILQSYNTALDWRKLRLOAFLP 182
 DB 112 NT-WSDEITQTKNIKKKEASTYISNANKILNRSFNVIYSTVYHNLKTWE-----NNENPQ 165
 QY 183 PSSALQQAULTKTRFENVDNDFREIP--GFQLETYKTLILPIYAAANFHLNLLQGA 240
 DB 166 NTQDVRTQIQLVHVHFQNVPELVNSCPFPNPSDCDYNNILVLSYAAQANLHLTVLNOAV 225

241 ELADENNADIHPSQIEPNAGTSDYYKLLKENTIPKYSNYCANTYREGINKLRNBP----- 295
 226 KFEAYLKNRQPDYLEP-LPTAIDYYPLVLTAKAIEDYTNVCVTYTKGILNLIKTPDNL 284
 296 -NMRWSIFNDYRRYMTITVLDTAQSFYDKYKDSIGRIGGKTKLTREIYITENPD 354
 285 GNINMNTYNTYRTKMTTAVLDLVALPNYDVGYPI-----GVQSELTREIYQV-LNFE 337
 355 RLTYLEIQPNLAIMEYNLTRSGLRFLFSFLDELIFYTKNRYGRLVGIANRRSTYA--- 411
 338 ESPYKY--DFQVEDSLTERP-HLFTWLDLSLNFYKAOITPNNFF-TSHYNNFHYTLDN 393
 412 TTGTEIYGBRTGPTTKTLIPESYKVSIVTRQVTPTPSPFPNIYFTINOIELYLNNSP 471
 394 ISQKSSVFGNHNVTDLKLSL--GLATNIYIFLLNVLISLDNKLYDNVNNISKMDPFFITNGT 451
 472 ---SNKLTYSAGGNLSNDKTTDFQPVKDCPKIINPNCPLPSVNSYSHILSQSLFNY- 527
 452 RLLEKELT-AGSGQITVDVNNKNIIFGLPKRRENGQNTLFFPTVDYNSHILSFKLSUP 510
 528 -SYKIGLALNILYTGALGWTSSVNRNNAISDKITWIPAIGKNSLDTNSKVIEGPGHTG 586
 511 ATYK-----TQVTFA--WTHSSVDPKNTIYTHLTOIPAVKANSLGTSKVVQSPGHTG 563
 587 GNLVYLSQGRLEITCRTPNSTQSYIRLYATNGAGNTLPLNISLTIPGVIGIPPORLNN 646
 564 GDLI--DFKDHFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIPGVAEL-GMALNP 620
 647 TFGSTNNNLOYDGFYQFPSTVTIPLNRNIFPIFNRAVY-SNSILIIDKIEPIPTSS 705
 621 TFGSTDTNLYKYDFQYLEFSNEVKFAPNQNISLVFNRSQVYNTTTLIDKIEFLPITRS 680
 706 VRQNRKQKLETTQTKINTFTNHTKNTLNIEATNYDID 744
 681 IREDREKQKLETVQQLINTFYANPIKNTLQSELTDYDID 719

RESULT 6
 AAP94035
 ID AAP94035 standard; protein; 1016 AA.
 AC AAP94035;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 30-MAY-1990 (first entry)
 XX Delta-endotoxin crystal protein.
 DE Delta-endotoxin; crystal protein; insecticide; pCC130;
 XX biological control agent.
 XX Bacillus thuringiensis; israelensis.
 XX BP296870-A.
 XX 28-DEC-1988.
 XX 24-JUN-1988; 88EP-00305772.
 XX 26-JUN-1987; 87US-00067653.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Eilar DJ, Ward ES;
 XX WPI; 1989-001322/01.
 DR N-PSDB; AAN93054.
 XX DNA fragment encoding insecticidal protein - obt'd. from Bacillus
 PT thuringiensis sub species israelensis, and used in microorganisms and
 PT plant cells.

```
XX Diaclosure; Page; 26pp; English.
PS
XX
CC The protein is encoded by an insert in plasmid pC130. The delta
CC endotoxin protein is insecticidal and can be used to control insect pests
CC esp. mosquitoes. See also AAP93715. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct DR field.) (Updated on 27-AUG-
CC 2003 to correct OS field.)
XX
XX Sequence 1016 AA;
SQ

Query Match 29.6%; Score 1157; DB 1; Length 1016;
Best Local Similarity 37.3%; Pred. No. 2.7e-83;
Matches 283; Conservative 130; Mismatches 282; Indels 64; Gaps 25;

QY 5 NNNEYELIDS--KNLSYPSNRNDHSRYPTNPNQPLQNTNYKEWLNMCQGTQYGDNF 62
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
6 NKNEYETLNASOKLANISNN---YTRYPIENSPKQLQSTNYKDWLNMCQNQYGGDF 61
QY 63 ETPASADTIAAVSAGTIVSGTLGAGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
62 ETFIDS---GELSAVTIVGTVLTGFGFTT---PLGL---ALIRFGTLIPVLPFAQDOS 111
QY 123 KTVMTQFIKMGEIFVDTPLTESI KQLQTLGSGFRQILQSYNTALDDWRKELQAPGLP 182
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
112 NT-WSDFITQTKNIIRKKEASTYISNANKILNRSFNVISTYHNHLKTWE-----NNPNPQ 165
QY 183 PSSALQQAALTKIRFENVHNDIFIREIP--GFQLETYKTLTLLPIYAAAFHNLILQOGA 240
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
166 NTQDVRTQIQLVHYHFQNVIPVNSCPNPSDCDYNNILVSSYAAQANHLTVLNQAV 225
QY 241 ELADEWNADIHPISOIRNACTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
226 KFAEYLNKNRQFDYLEP-LPTAIDYIPVLTKAIEDYTNVCVTTKYKGLNLIKTTPDSNLD 284
QY 296 -NMRWSIFNDYRYMTITVLDITIAQFSFYDIKRYKDSIGRIGIKTELREIYTTBEINF 354
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
285 GNINMNTYNTYRTKMTAVLDVVALFPNDYGVKPI-----GVQSELTREIYQV-LNFE 337
QY 355 RLTYLEIQPNLAIMEYNTLRSGIRLFSFLDELIFTYKNETYGNRLVGIANRSTYA---411
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
338 ESPYKYY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQTTNNFF-TSHYNNFHYTLDN 393
QY 412 TTGTEIYIGERTGPPTTKTLIPFESYKYSIVTDQVTPSPFPNIYFTTNQIELYLNNSP 471
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
394 ISQKSSVFGNHNVTDKLKS--GLATNIYIFLNLVSLDNKYLNNDYNNISKMDFFITNGT 451
QY 472 ---SNKLTYSAGGNLSNDKTTDFQFPVKDKCPPIINPNCLPSYNSYSHLSQFSLENY-527
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
452 RLLEKELT-AGSGQITVDVKNKIFGLPKLRRENQGNPTLFTYDNYSHLSIFKSLSIP 510
QY 528 -SYKIGLALNLYTGALGWHSSVNRNALSDKIITWIPA KNSLDTSKSVKEGPGHTG 586
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
511 ATYK-----TQVYTFE--WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQFGHTG 563
QY 587 GNLVYLQSGRLEITCRTPNSTQSYIRLRYATNGAGNTLPNLSLITPGVIGIPQORLNN 646
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
564 GDLI--DFKHDFKLTQHSNFQSYFIRIRYAGSGANTRAVNLSPGVAEL-GNALNP 620
QY 647 TFSGTNNNLQYDGFQYFPFSTVTLPLNRIIPFIENRADV-SNSILIIDKIEFIPITS 705
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
621 TFSGTDYTNLYKQDFQYLEFSEVNEKVPAPQNISLVFNRSVDYTNNTVTLIDKIEFLPITS 680
QY 706 VRONREKQKLETTQTKINTFTNHTKNTLNIEATNTDID 744
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
681 IREDREKQKLETVQOIINTFYANPKNLTQSELTDYDID 719

RESULT 7
AAP82589
ID AAP82589 standard; protein; 1180 AA.
XX
XX
,AC AAP82589;
```

```
XX 24-OCT-2003 (revised)
DT 05-NOV-1990 (first entry)
XX
XX Insecticidal (Diptera) protein (exon 2).
DE
XX Insecticidal protein gene; Diptera; Aedes.
KW
XX Bacillus thuringiensis serovar israelensis.
OS
XX JP63230090-A.
PN
XX 26-SEP-1988.
XX
XX 19-MAR-1987; 87JP-00066844.
PF
XX 19-MAR-1987; 87JP-00066844.
PR
XX (SUMO ) SUMITOMO CHEM IND KK.
PA
XX WPI; 1988-311968/44.
DR N-PSDB; AAN81490.
XX
XX New insecticidal protein of bacillus thuringiensis israelensis strain -
PT prepd. by isolating plasmid contg. insecticidal protein gene by forming
PT gene library from plasmid deoxyribonucleic acid, etc.
XX
XX Disclosure; Page ?; 9pp; Japanese.
PS
XX A plasmid contg. the gene is isolated by forming a gene library from
CC plasmid DNA of B.thuringiensis israelensis (HD 522 strain, USA Goldberg
CC ONR60) followed by screening with anti-israelensis insecticidal protein
CC IG. The insecticidal protein is highly effective against Diptera, esp.
CC Aedes. See also AAP81034. (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 1180 AA;
SQ

Query Match 29.6%; Score 1157; DB 1; Length 1180;
Best Local Similarity 37.3%; Pred. No. 3.4e-83;
Matches 283; Conservative 131; Mismatches 281; Indels 64; Gaps 25;

QY 5 NNNEYEIDS--KNLSYPSNRNDHSRYPTNPNQPLQNTNYKEWLNMCQGTQYGDNF 62
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
6 NKNEYETLNASOKLANISNN---YTRYPIENSPKQLQSTNYKDWLNMCQNQYGGDF 61
QY 63 ETPASADTIAAVSAGTIVSGTLGAGLTSISGPIGIIIGAIISFGTLITVFWPAGEQD 122
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
62 ETFIDS---GELSAVTIVGTVLTGFGFTT---PLGL---ALIRFGTLIPVLPFAQDOS 111
QY 123 KTVMTQFIKMGEIFVDTPLTESI KQLQTLGSGFRQILQSYNTALDDWRKELQAPGLP 182
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
112 NT-WSDFITQTKNIIRKKEASTYISNANKILNRSFNVISTYHNHLKTWE-----NNPNPQ 165
QY 183 PSSALQQAALTKIRFENVHNDIFIREIP--GFQLETYKTLTLLPIYAAAFHNLILQOGA 240
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
166 NTQDVRTQIQLVHYHFQNVIPVNSCPNPSDCDYNNILVSSYAAQANHLTVLNQAV 225
QY 241 ELADEWNADIHPISOIRNAGTSDDYKLLKENIPKYSNYCANTYRGLNKLNEP-----295
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
226 KFEAVLNKNRQFDYLEP-LPTAIDYIPVLTKAIEDYTNVCVTTKYKGLNLIKTTPDSNLD 284
QY 296 -NMRWSIFNDYRYMTITVLDITIAQFSFYDIKRYKDSIGRIGIKTELREIYTTBEINF 354
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
285 GNINMNTYNTYRTKMTAVLDVVALFPNDYGVKPI-----GVQSELTREIYQV-LNFE 337
QY 355 RLTYLEIQPNLAIMEYNTLRSGIRLFSFLDELIFTYKNETYGNRLVGIANRSTYA---411
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
338 ESPYKYY--DFQYQEDSLTRP-HLFTWLDLSNFYEKAQTTNNFF-TSHYNNFHYTLDN 393
QY 412 TTGTEIYIGERTGPPTTKTLIPFESYKYSIVTDQVTPSPFPNIYFTTNQIELYLNNSP 471
Db ||||| : : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
394 ISQKSSVFGNHNVTDKLKS--GLATNIYIFLNLVSLDNKYLNNDYNNISKMDFFITNGT 451
```



```

XX 26-JAN-1995.
XX
XX
XX 13-JUL-1994; 94WO-US007902.
XX
XX 15-JUL-1993; 93US-00093199.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Hickie LA, Payne J;
XX
XX WPI; 1995-067338/09.
XX
XX N-PSDB; AAQ81178.
XX
XX Method for controlling Calliphoridae pests - specifically utilises
XX Bacillus thuringiensis isolates or toxins.
XX
XX Disclosure; Page 36-38; 50pp; English.
XX
XX A library was constructed from Bacillus thuringiensis PS7IM3 total
XX cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia
XX coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This
XX was sequenced (AAQ81178). A cured, acrystalliferous B.t. host carrying
XX pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to
XX calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 1180 AA;
XX
XX
XX Query Match 29.5%; Score 1153; DB 2; Length 1180;
XX Best Local Similarity 37.2%; Pred. No. 7.2e-83;
XX Matches 282; Conservative 131; Mismatches 282; Indels 64; Gaps 25;
XX
XX 5 NNNEYELIDS--KNLSFSPNRNDHSRYPYTNPNQPLQNTYKELWLMCOGHTQYGDNF 62
XX | | | | : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 6 NKNEYELNASQKKLNSN-----YTRYPIENSFKQLQSTNYKDLNLMCQQQYGGDF 61
XX
XX 63 ETPASADTAAVAGTIVSGTLGAGLTSISGPIGIIIGAIISFGTLITVWPAGEOD 122
XX | | | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 62 ETFIDS---GELSAITIVGTLTGFTT---PLGL---ALIGFTLIPVLFPAQDQS 111
XX
XX 123 KTWVQPIKNGEIVDPPLTESIKQLKLTLEGFRQILOSYNTALDDWRKRLQAPGLP 182
XX | : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 112 NT-WSDFITQTKIIKEASTVISNANKILNRSFNVISYTHNLKTWE-----NNPNPQ 165
XX
XX 183 PSSALQQAALTAKIRENVHNDIREIP--GFQLETYKTLLLPIYAQAANFHLNLQOGA 240
XX
XX 166 NTQDVRTQIOLVHYHFQNVIPELVNSCPNPSPDCDYNILVLSYQAQAANLHLTVLNQAV 225
XX
XX 241 ELADEWNADTHPSQIEPNAGTSDDYKLLKENIPKYSNYCANTYREGNKLKNRP----- 295
XX : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 226 KFEAYLKNNRQFDYLEP-LPTAIDYYPVLTKAIEDYTNVCVTKYKGLNLIKTPPSNLD 284
XX
XX 296 -NMRWSIFNDYRYMTITVLDTTAQPSFYDIKRYKDSIGRIGIKTELTRBIYTTSEINF 354
XX | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 285 GNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYP-----GVQSELTRIIYQV-LNFE 337
XX
XX 355 RLTYLEIQPNLAMEYNLTSGRLSPFLDELIFYTKNEYGNRLVGIANRSTYA--- 411
XX | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 338 ESPYKYV--DFQVQESLSTRP-HLFTWLDLSLNFYEKAQTPPNFF-TSHYNNFHYTLDN 393
XX
XX 412 TTGTETIYIGRTGPPTTKTILIPESYKVSIVTDQVTPTPSPFPNIYFTINQIELYLNNSP 471
XX | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 394 ISQKSSVFGNHNVTDLKSL--GLATNIYIFLNLVSLDNKYLNDYNNISKMDFFITNGT 451
XX
XX 472 ---SNKLTYSAGNLSNDKXTTDFQPPVKDCKPPIPNPCLPSYNSYSHILSIFSIFYN- 527
XX | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 452 RLLEKELT-AGSQITVDYVKNKIFGLPIKLPRENQAIPTLFTPYDNYSHILSPIKLSIP 510
XX
XX 528 -SYKIGLALNLYTGALGWTHSSVNRNNAISDKIITWIPAKNSLDTWKVLGEGHGTG 586
XX | : : : | | | : : : | | | : : : | | | : : : | | | : : :
XX 511 ATYK-----TQVYTF--WTHSSVDPKNTIYTHLTQIIPAVKANSLGTSKVVQGGHGTG 563
XX
XX 587 GNLVYLSQGRLEITCTPNSTQSYIRLRYATNGAGNTLPNLISLTIPGVIGIPQRLNN 646

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Db 564 GDLI--DFKDHFKITCOHSNFOQSIFIRIRYASNGSANTRAVINLSIPGVAEL-GNALNP 620
| : | : : : : : : : | : | : | : | : | : | : | : | : | : | : | :
Qy 647 TFSGTNNYNNLQYDFGYFOFPSTVTPLFLNRNIPFPINRADV-SNSLIILDKIEFIPITGS 705
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 621 TFSGTDYTNLKYKDKFOYLEFSNEVAFAPNQNLISLVFNRSDDVTNTTTLVDKIEFLPITRS 680
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 706 VRQNRKQKLETTQYKINTFFTNHTKNTLNIENATNYDID 744
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 681 IREDREKQKLETVQOIINTFYANPIKNTLQSELTDYDID 719
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 10
AAE26353
ID AAE26353 standard; protein; 1109 AA.
XX
XX AAE26353;
XX
XX 13-DEC-2002 (first entry)
XX
XX Bacillus thuringiensis ssp. finitimus cry28Aa1 delta-endotoxin.
XX
XX Delta-endotoxin; cry26Aa1; cry28Aa1; insect-resistant plant; toxin;
XX transgenic host cell; insecticide.
XX
XX Bacillus thuringiensis.
XX
XX US2002038005-A1.
XX
XX 28-MAR-2002.
XX
XX 08-JAN-2001; 2001US-00756526.
XX
XX 07-JAN-2000; 2000US-0175158P.
XX
XX (WOJC/) WOJCIECHOWSKA J A.
XX (LEWI/) LEWITIN E I.
XX (ZALU/) ZALUNIN I A.
XX (REVU/) REVINA L P.
XX (CHES/) CHESTUKHINA G G.
XX
XX Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
XX Chestukhina GG;
XX
XX WPI; 2002-403936/43.
XX N-PSDB; AAD43974.
XX
XX Novel isolated delta-endotoxin nucleic acid molecules, cry26Aa1 and
XX cry28Aa1 isolated from Bacillus thuringiensis finitimus, that encodes
XX toxin active against insects, useful for controlling insects.
XX
XX Claim 1; Page 37-40; 42pp; English.
XX
XX The invention relates to isolated delta-endotoxin nucleic acid molecules,
XX cry26Aa1 and cry28Aa1 isolated from Bacillus thuringiensis finitimus,
XX that encode a toxin that is active against insects. The invention is
XX useful for producing an insect-resistant plant, by introducing the
XX nucleic acid molecule into the plant, where the nucleic acid is
XX expressible in the plant in an effective amount to control an insect. The
XX invention is useful for producing a toxin that is active against insects
XX by obtaining the transgenic host cell and expressing the nucleic acid
XX molecule in the host cell, which results in the toxin that is active
XX against insects. The toxin is useful for controlling an insect by
XX delivering to the insect an effective amount of toxin. The invention is
XX useful for controlling insects. The toxin is useful for inhibiting the
XX ability of insect pest to survive, grow or reproduce, for limiting insect
XX related damage or loss in crop plants, and to prophylactically treat
XX insect susceptible areas or crops plants, to confer protection or resistance
XX against harmful insects. The present sequence is Bacillus thuringiensis
XX ssp. finitimus cry28Aa1 delta-endotoxin
XX
XX Sequence 1109 AA;

```

```
Query Match      23.1%; Score 901; DB 5; Length 1109;
Best Local Similarity 34.2%; Pred. No. 1.2e-62;
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;

Qy 67 SADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGQD-KTV 125
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPBEDPKKI 80
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 126 WTQIKMGEIFVDTPLTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQLAQGLPPSS 185
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 WSQFMKGEDLLNQITISAVKESIALAHNLGPKDVLTYTTERAFNDWKR-----NPSA 131
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 186 ALQQAALTLRPNVNDFTREIPGFOLEYTKTLLPIYAQAANFHLNLQCGAEADE 245
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 132 ---NTARLVSRQFENAHFNFVSNMPLQLPTDYLTLSCYTEAAANLHLNLHQGVQFADQ 188
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 246 WNADHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGKLNKRNPNRWSIFNDY 305
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 189 WNADQPHSPMLKSSGT---YYDELLVYIEKYINCYTKTYHKLHKLSEKIKITWDVNTY 245
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 306 RRYMTITVLDIAOFSFYDIKRYKDSIGRIGIKTELTREIYTTINFDRLTYLEIOPNL 365
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 246 RREMTLIVDLVATFPFDIRFP-----RGVELELTREYVTS-----LDHLTRPG- 292
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 366 AIMEYNLTRSLGRLPFSFDELIFYTKNETYGNRLVIGIANRNRSTVATGTETI-----IYG 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 293 -----LFTWLSDELTYTESVAEGDYLSGI-----RESKYVTGNQFTWKNIYG 335
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 ERTGPPTTK-----TLIPFESYKVSIVTDQVTFTPFPNIFTINQIELYLNNSPNK 474
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 530 KIGLALNLTGALGTHSSVNRNNAISDKIITWIPAIKGNSLDNTSKVIEGPGHTGNL 589
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 434 EFAYFHSIF--ALGWTNHSVNSQNLISESVSTQIPLVAYEV--TNNSVIRGPGTGGDL 490
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 590 VYLOSQGRLEITCRTPNSTQSYIIRLVATNGAGNTLPLNISLTIPGVIGIPQRLNNTFS 649
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 491 IELRD--KCSIKCKA--SSLKKYASLSFYAANNAIVSIVDGDGAGVL-----LQPTFS 541
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 650 GTNYYN-----LOYDGFQFQFPSTVTLPLNRNIPFIFNRAD--VNSILIIDKIEFTPI 702
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 542 RKGNNFTIQDLNKDFQYHTLLVDIELPESEEHILHKLREDDYEEGVILLIDKLEFKPI 601
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 703 TSSVRQNRKOKLETIOQTINTFFTNHTKNTLNIEATNYDID 744
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 602 DENY---TNEWNLEKAKKAVNVLFINAT--NALKMDVTDYHID 639
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ADF31302
ID ADF31302 standard, protein; 1109 AA.
XX AC ADF311302;
XX AC ADF311302;
XX DT 12-FEB-2004 (first entry)
XX DE Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
XX KW Cry28Aa1; delta-endotoxin; insect pest control;
XX KW transgenic plant; insect resistance; insecticide.
XX OS Bacillus thuringiensis serovar finitimus.
XX PN US2003150018-A1.
XX PD 07-AUG-2003.
XX PF 15-JAN-2003; 2003US-00345020.

XX 07-JAN-2000; 2000US-0175158P.
PR 08-JAN-2001; 2001US-00756526.
XX (WOJC/) WOJCIECHOWSKA J A.
PA (LEWY/) LEWITIN E I.
PA (ZALU/) ZALUNIN I A.
PA (REVI/) REVINA L P.
PA (CHES/) CHESTUKHINA G G.
PI Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
PI Chestukhina GG;
XX WPI; 2003-897623/82.
DR N-PSDB; ADF31301.
XX New isolated nucleic acid molecule encoding a toxin that is active
PT against insects useful for controlling insect pests or for conferring
PT insect resistance in plants.
XX Claim 22; SEQ ID NO 4; 42pp; English.
XX The present invention relates to the isolation of novel cry26Aa1 and
CC cry28Aa1 delta-endotoxin genes from Bacillus thuringiensis ssp.
CC finitimus. The sequences for the delta-endotoxin polypeptides are also
CC disclosed. The invention provides methods for producing the toxins and
CC compositions containing the toxins. The methods and sequences of the
CC invention are useful for controlling insect pests in transgenic plants to
CC confer insect resistance. The present sequence represents the cry28Aa1
CC delta-endotoxin of the invention.
XX Sequence 1109 AA;

Query Match      23.1%; Score 901; DB 7; Length 1109;
Best Local Similarity 34.2%; Pred. No. 1.2e-62;
Matches 240; Conservative 106; Mismatches 242; Indels 114; Gaps 27;

Qy 67 SADTIAAVSAGTIVSGTLLAGIGLTSISGPIGIIIGAIISFGTLITVFWPAGQD-KTV 125
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 28 SSDTAVVVSAGIVVVGITLT---AFASFVNP---GVVLISFGTLAPVLPDPBEDPKKI 80
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 126 WTQIKMGEIFVDTPLTESIKQLKLTLEGFRQLQSYNTALDDWRKLRQLAQGLPPSS 185
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 WSQFMKGEDLLNQITISAVKESIALAHNLGPKDVLTYTTERAFNDWKR-----NPSA 131
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 186 ALQQAALTLRPNVNDFTREIPGFOLEYTKTLLPIYAQAANFHLNLQCGAEADE 245
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 132 ---NTARLVSRQFENAHFNFVSNMPLQLPTDYLTLSCYTEAAANLHLNLHQGVQFADQ 188
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 246 WNADHPSQIEPNAGTSDDYKLLKENIPKYSNCANTYREGKLNKRNPNRWSIFNDY 305
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 189 WNADQPHSPMLKSSGT---YYDELLVYIEKYINCYTKTYHKLHKLSEKIKITWDVNTY 245
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 306 RRYMTITVLDIAOFSFYDIKRYKDSIGRIGIKTELTREIYTTINFDRLTYLEIOPNL 365
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 246 RREMTLIVDLVATFPFDIRFP-----RGVELELTREYVTS-----LDHLTRPG- 292
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 366 AIMEYNLTRSLGRLPFSFDELIFYTKNETYGNRLVIGIANRNRSTVATGTETI-----IYG 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 293 -----LFTWLSDELTYTESVAEGDYLSGI-----RESKYVTGNQFTWKNIYG 335
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 ERTGPPTTK-----TLIPFESYKVSIVTDQVTFTPFPNIFTINQIELYLNNSPNK 474
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 336 N-----TNRLSKQLITLLPGE-FMTHLSINRPPQTIAINKLYSLIQKI---VFTTFKND 386
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 475 LYSAGGNLND---KKTTFDQFPVKDCKPIINPCLPSVNS--YSHLSQFSLEFVSY 529
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 387 NEYQKNFNVNQNPEQETNY-----PNDYGGNSQKFKNLSHFFLIHKL 433
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 530 KIGLALNLTGALGTHSSVNRNNAISDKIITWIPAIKGNSLDNTSKVIEGPGHTGNL 589
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 434 EFAYFHSIF--ALGWTNHSVNSQNLISESVSTQIPLVAYEV--TNNSVIRGPGTGGDL 490
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 590 VYLOSQGRLEITCRTPNSTQSYIIRLVATNGAGNTLPLNISLTIPGVIGIPQRLNNTFS 649
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 491 IELRD--KCSIKCKA--SSLKKYASLSFYAANNAIVSIVDGDGAGVL-----LQPTFS 541
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 650 GTNYYN-----LOYDGFQFQFPSTVTLPLNRNIPFIFNRAD--VNSILIIDKIEFTPI 702
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 542 RKGNNFTIQDLNKDFQYHTLLVDIELPESEEHILHKLREDDYEEGVILLIDKLEFKPI 601
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 703 TSSVRQNRKOKLETIOQTINTFFTNHTKNTLNIEATNYDID 744
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 602 DENY---TNEWNLEKAKKAVNVLFINAT--NALKMDVTDYHID 639
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
Cry28Aa1; delta-endotoxin; insect pest control;
transgenic plant; insect resistance; insecticide.
Bacillus thuringiensis serovar finitimus.
US2003150018-A1.
07-AUG-2003.
15-JAN-2003; 2003US-00345020.
```


XX WPI; 1995-067338/09.
 DR N-PSDB; AAQ81180.
 XX Method for controlling Calliphoridae pests - specifically utilises
 PT Bacillus thuringiensis isolates or toxins.
 XX
 PS Disclosure; Page 42-43; 50pp; English.
 XX
 CC A library was constructed from Bacillus thuringiensis PS71M3 total
 CC cellular DNA in lambda Gem-11. Plasmid pMVC1636, selected in Escherichia
 CC coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was
 CC sequenced (AAQ81180). A cured, acrycallyiferous B.t. host carrying
 CC pMVC1636 produced a 77 kDa crystal protein (AAR63079). (Updated on 25-MAR
 CC -2003 to correct PN field.)
 XX
 SQ Sequence 686 AA;
 Query Match 23.0%; Score 900; DB 2; Length 686;
 Best Local Similarity 32.9%; Pred. No. 6.8e-63;
 Matches 251; Conservative 115; Mismatches 268; Indels 128; Gaps 32;
 QY 5 NNEVEIIDSKNLSYPSNRNIDHSRYPTNNPNQPLONTNYKEWLNMCQGNTOYQDNFET 64
 DB 6 NKNEYEIFNPSNGFSKSN--YSRYPLANKPNQPLONTNYKOWLNVCQDNQOYGNAGN 63
 QY 65 PASADTIAAASAGTIVSGTLLAGIGLTSISGPIIGIICAIISFGTLITVFWPAGEQDKT 124
 DB 64 FVSSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLIPFW-QGSDPAN 114
 QY 125 VWTQFIKMGEIFVDTPLTE---SIKQLKLTLEGFRQILQSYNTALDWRKLEQLQAPGL 181
 DB 115 VWDLLNIG---GRPIQIEDKNIINVLTVIPVPIKNQDKYQEFFDKWEPAR----- 163
 QY 182 PPSALOQAALTUKIRENVHN---DFIREIPGQLETYKTLPIYAQAANFHLNLLQ 238
 DB 164 --THANAKAVHDLFTTLEPIIDKOLDMLKNASYRIPT-----LPAYAQAATWHLNLLKH 216
 QY 239 GAELADENWADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGINKLRNPNM 297
 DB 217 AATYNIW---LQNGINPSTFNSNYQYGLKRIQIETDYCIQTYNAGLTWIRTNTA 273
 QY 298 RWSIFNRYRMTVLDTIAQFSFYDIKRYKDSIGRIGGKIBELTREIYVTEINFRLT 357
 DB 274 TWNYNTYRLTMLTLDLIAFPNDPEKYP-----GVKSLTREVY-TNVNSDTER 326
 QY 358 YLETOPNLAINENYLRSGLEFLSFLDELIEPTKN-----ETY-----GNRLVGIANRN 406
 DB 327 -----TITELNGLTRNP-TLFTWINGQFRYTRNSRDILDPYDIFSGTGNQMA----- 373
 QY 407 RSTVATTGTEIYBERTG---PPTTKTLIPESY---KVSIVTDROVTPSPFPNIYFT 459
 DB 374 -FTWINDRNIWGANVGHIIISQTSKVPFPRKPKDKVEIVHRE-----YSD 422
 QY 460 INQIELYNLSPSKLTYSAGNLSNDKTTDFOPVKOCKPIINPNCLPSYNSYSHIL 519
 DB 423 IIVEMIFPNS-SEVFRYSSNTIENNYKRTDSYMPKQTKW-----NKSYGHTL 471
 QY 520 SQPSLFNYSYKIGLAINILYTGALGWTHSSVNRNNAISDKLITMIPAKNSLDTNSKVI 579
 DB 472 SYIKTDNYFVS---VRRRRVAFSWTHTSVDFQNTIDLDNITQIHALKALKVSSDSKIV 528
 QY 580 EGPHTGGLVLOSQGRLEITCR-TPNSTOSYIRLRYATNGAGNTLPNISLIPGVIG 638
 DB 529 KGPHTGGDLVILKDS--MDPRVFLKNVSRQYQVIRYATNA-----PKTVFVLGIDT 581
 QY 639 IPPORLNNFTSGTNYN--NLQYDGFYQFPSTV-----TLPNLRNIPFIRNADV 687
 DB 582 ISVE-LPSTTSKQPNATDLTADYDFGVYFPRTPVNTKTFEGEDTLLMT-----LYGTPNH 635
 QY 688 SNSLIIDKIBFIPITSSVRNQRKQLETTQTKINTFFTH 729
 DB 636 SYNI-YIDKIEFIPITQSVDLTEKONIEKTKQKIVNDLFVNN 676

RESULT 14

AAR14374

XX AAR14374 standard; protein; 675 AA.

XX AAR14374;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 04-FEB-1992 (first entry)

XX Dipteran active toxin.

XX Insecticide; B.t; crystal; delta endotoxin; cryIVC.

XX Bacillus thuringiensis serovar morrisoni.

XX EP457498-A.

XX 21-NOV-1991.

XX 09-MAY-1991; 91EP-00304180.

XX 15-MAY-1990; 90US-00524255.

PR 01-OCT-1990; 90US-00590903.

XX (MYCO) MYCOGEN CORP.

XX Sick AJ;

XX WPI; 1991-341902/47.

DR N-PSDB; AAQ14670.

XX Bacillus thuringiensis genes encoding diptera-active toxins - and

XX transformed microbes used to control insects in various environments.

XX Claim 3; Page 15; 20pp; English.

XX The sequence was deduced from the DNA sequence obt'd. from plasmid

XX pMVC1636 which was isolated from a genomic library prep'd. from DNA from

XX B.t. PS71M3 [from B.t. PS71M3-69 (NRRL B-18515)]. It is related to the

XX cryIVC toxins from B.t. var. israelensis. The protein has a mol. wt. of

XX 77 kD. Microorganisms transformed with the DNA may be administered to

XX dipteran insects or their environ- ments, the expressed toxins acting as

XX an insecticide. See also AAR14373. (Updated on 25-MAR-2003 to correct PA

XX field.) (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 675 AA;

Query Match 23.0%; Score 899; DB 2; Length 675;

Best Local Similarity 33.0%; Pred. No. 7.9e-63;

Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

QY 5 NNEVEIIDSKNLSYPSNRNIDHSRYPTNNPNQPLONTNYKEWLNMCQGNTOYQDNFET 64

DB 6 NKNEYEIFNPSNGFSKSN--YSRYPLANKPNQPLONTNYKOWLNVCQDNQOYGNAGN 63

QY 65 PASADTIAAASAGTIVSGTLLAGIGLTSISGPIIGIICAIISFGTLITVFWPAGEQDKT 124

DB 64 FVSSETIVGSAGIIVVGTMLG-----AFAAP--VLAAGIISFGTLIPFW-QGSDPAN 114

QY 125 VWTQFIKMGEIFVDTPLTE---SIKQLKLTLEGFRQILQSYNTALDWRKLEQLQAPGL 181

DB 115 VWDLLNIG---GRPIQIEDKNIINVLTVIPVPIKNQDKYQEFFDKWEPAR----- 163

QY 182 PPSALOQAALTUKIRENVHN---DFIREIPGQLETYKTLPIYAQAANFHLNLLQ 238

DB 164 --THANAKAVHDLFTTLEPIIDKOLDMLKNASYRIPT-----LPAYAQAATWHLNLLKH 216

QY 239 GAELADENWADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTYREGINKLRNPNM 297

DB 217 AATYNIW---LQNGINPSTFNSNYQYGLKRIQIETDYCIQTYNAGLTWIRTNTA 273

Db 529 KGPHTGGDLVILKDS--MDFRVRFKNVSRQVIRIRATNA-----PKTTVFLTGIDT 581
Qy 639 IPPQRLNNTFSGTNYN--NLQYGDGFGYFQPPSTV-----TLPLNRNIPFIENRADV 687
Db 582 ISVE-LPSTTSRQNPATDLTYADFGYVTFPRTVPNKTPGEDTLLMT-----LYGTPNH 635
Qy 688 SNSILIIDKIEFIPITSSVRQNRKQKLETIQTKINTFFTN 728
Db 636 SYNI-YIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFVN 675

Search completed: December 15, 2005, 10:50:59
Job time : 194 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 10:44:23 ; Search time 232 Seconds
(without alignments)
2262.556 Million cell updates/sec

Title: US-10-782-570-2

Perfect score: 3906

Sequence: 1 MNQNNNEYIISKNLSYP.....FFTNHTKNTLNIEATNYDID 744

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1158	29.6	1180	1	CR4AA_BACTI
2	1158	29.6	1180	2	Q7AL67_BACTI
3	906.5	23.2	1128	2	Q9FDC0_BACTF
4	901	23.1	1109	1	C28AA_BACTF
5	897	23.0	675	1	C10AA_BACTI
6	897	23.0	675	2	Q8KNV2_BACTI
7	843	21.6	650	2	Q8VNX2_BACTV
8	819	21.0	1136	1	CR4BA_BACTI
9	819	21.0	1136	2	Q7AL72_BACTI
10	802	20.5	688	2	Q8VNX1_BACTV
11	796	20.4	683	2	Q75VA2_BACTE
12	791.5	20.3	1169	1	CR8BA_BACUK
13	755.5	19.3	688	2	Q7W7N9_BACTU
14	712.5	18.2	1169	2	Q56B08_BACTU
15	710	18.2	659	1	CR3BA_BACTO
16	709.5	18.2	682	1	C19BA_BACUH
17	703	18.0	829	2	Q8BE06_BACTU
18	695	17.8	652	1	CR3BB_BACTU
19	693	17.7	1138	1	CR7AB_BACUK
20	692	17.7	1138	1	CR7AA_BACTU
21	690	17.7	825	2	Q6BE09_BACTU
22	689	17.6	648	1	C19AA_BACTJ
23	687	17.6	660	2	Q8R0U6_BACTA
24	686.5	17.6	1236	2	Q339P3_BACTU
25	684	17.5	1280	2	Q8VUK9_BACTU
26	681.5	17.4	1157	1	CR8AA_BACTU
27	676	17.3	1160	1	CR8CA_BACTP
28	676	17.3	1160	2	Q6R2R6_BACTU
29	665	17.0	1138	1	CR7AB_BACUA
30	660	16.9	686	2	Q75Q05_BACTE
31	659.5	16.9	1157	1	CR9CA_BACTO

32	658.5	16.9	1163	2	Q5XLA8_BACTP	Q5XLA8 bacillus th
33	656	16.8	1169	1	CR9DA_BACTP	Q6014 bacillus th
34	640.5	16.4	1144	2	Q8KZL7_BACTG	Q8KZL7 bacillus th
35	639	16.4	1154	2	Q6QAN9_BACTG	Q6QAN9 bacillus th
36	635	16.3	1254	2	Q8VULO_BACTG	Q8VULO bacillus th
37	630	16.1	826	1	C27AA_BACUH	Q8E597 bacillus th
38	629	16.1	1150	1	CR9EA_BACTA	Q9ZNL9 bacillus th
39	629	16.1	1150	2	Q7IRP4_BACTU	Q7IRP4 bacillus th
40	627.5	16.1	1231	2	Q8KNY2_BACTU	Q8KNY2 bacillus th
41	620.5	15.9	644	1	CR3AA_BACTD	Q8K381 bacillus th
42	620.5	15.9	644	1	CR3AA_BACTM	Q8K380 bacillus th
43	620.5	15.9	644	1	CR3AA_BACTT	Q8K379 bacillus th
44	620.5	15.9	652	2	Q9S6N9_BACTU	Q9S6N9 bacillus th
45	620.5	15.9	1231	1	CR1BD_BACTZ	Q9ZAZ5 bacillus th

ALIGNMENTS

RESULT 1

ID	CR4AA_BACTI	STANDARD;	PRT;	1180 AA.
AC	PI6480;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DB	Pesticidal crystal protein cry4Aa (Insecticidal delta-endotoxin CryIVA(a)) (Crystalline entomocidal protoxin) (135 kDa crystal protein).			
GN	Name=cry4Aa; Synonyms=cryIVA(a), isrH4;			
OS	Bacillus thuringiensis subsp. israelensis.			
OG	Plasmid 72 Kb.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;			
OC	Bacillus cereus group.			
OX	NCBI_TaxID=1430;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Sen K., Honda G., Koyama N., Nishida M., Sakai H., Himeno M., Komano T.;			
RT	"Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis.";			
RL	Agric. Biol. Chem. 52:873-878(1988).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88015571; PubMed=2821500;			
RA	Ward E.S., Ellar D.J.;			
RT	"Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding a 130 kDa delta-endotoxin.";			
RL	Nucleic Acids Res. 15:7195-7195(1987).			
RN	[3]			
RP	MUTAGENESIS STUDIES.			
RX	MEDLINE=94307434; PubMed=7913448; DOI=10.1016/0014-5793(94)00604-0;			
RA	Nishimoto T., Yoshisue H., Ihara K., Sakai H., Komano T.;			
RT	"Functional analysis of block 5, one of the highly conserved amino acid sequences in the 130-kDa CryIVA protein produced by Bacillus thuringiensis subsp. israelensis.";			
RL	FEBS Lett. 348:249-254(1994).			
CC	-1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut epithelial cells of insects.			
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.			
CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.			
CC	-1- MISCELLANEOUS: Diverse amino acid mutations in sequence block 667-676 have no direct effect on the insecticidal activity but alter the structural stability of the toxin protein molecule.			
CC	-1- SIMILARITY: Belongs to the delta endotoxin family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			


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Db 472 SYIKTDNYIFSV---VRERRVAFSWTHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLOSQRLEITCR--TPNSTQSYVIRLYATNGAGNTLPNISLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDPRVFLKNVSRQVQVIRIYATNA-----PKTTVLTGIDT 581
Qy 639 IPPORLANTFSGTNYN--NLQYGDGYFQFPSTV-----TLPLNRNIPFIFNRADV 687
Db 582 ISVE-LPSTTSRQPNATDLTYADFGVYTFPRTPVNTKTFEGEDLLMT-----LYGTPNH 635
Qy 688 SNSILIIDKIEFIPITSSVRQNRKQKLETTQTQKINTFFTN 728
Db 636 SYNI-YIDKIEFIPITQSVDLYTEKQIEKTKIVNDLVFN 675

RESULT 6
Q8KV2 BACTI
ID Q8KV2 BACTI PRELIMINARY; PRT; 675 AA.
AC Q8KV2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidicidal crystal protein cry10AA.
GN Name=cry10AA; Synonyms=cryIVC, cryXA(A), pBt047;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22235415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL731825; CAD30098.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 675 AA; 77759 MW; 4BB0B51AA0372FF1 CRC64;

Query Match 23.0%; Score 897; DB 2; Length 675;
Best Local Similarity 33.0%; Pred. No. 2.1e-48;
Matches 251; Conservative 114; Mismatches 268; Indels 128; Gaps 32;

Qy 5 NNNYEIIDSKNLSYPSNRNIDHSRYPTNNPQNTNYKEWLNMCQGNQYQDNFET 64
Db 6 NKNYEIIFNAPSNGFSKSN--YSRYPLANKPNQPLKNTNYKDLNVQDNQYGNNA 63
Qy 65 FASADTTAASAGTIVSGTLLAGTSGTSGPITGIGIIGIISFGTILTVFWPAGEQDKT 124
Db 64 FASSETTVGSAGIIVGVTMLG-----AFAAP--VLAAGIISFGTLLPIFW-QGSDPAN 114
Qy 125 VWTQFIKMGFEIVDTPLTE---SIKQKLTQLEGFROILOSNTALDWRKLRQLAPGL 181
Db 115 VWQDLNIG-----GRPTQIEDKNILNVLTISVTPIKNQDKYQEFFKWEPRAR----- 163
Qy 182 PPSSALQQAALTAKIRFENVHN---DFIREIPGQLEYTKTLLPIYAQAANFHLNLLQ 238
Db 164 --THANAKAVHDLFTTLEPIIDKDLMLKNNASYRIPT-----LPAYAQAIAFWHLNLLKH 216
Qy 239 GAELADFNWADIHPSQIEPNAGTSDDYK--LLKENIPKYSNYCANTREGINKLRNPNM 297
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Db 217 AATYNIW---LQOQINPSTFNSNYYQGYLKRKIOEYTDYCIQTNAGTUMIRTWNA 273
Qy 298 RWSIFNDYRYMTITVLDTIAQSFYDIKRYKDSIGRIGIKTELTREIYTFEINFDRLT 357
Db 274 TNNYNTYRLTEWLTVLDTIAIPNYPEKPI-----GVKSELIREVY-TNVSDFTR 326
Qy 358 YLSIQPNLAIMEYNLTRSGRLFSFLDELIFYKN-----ETY-----GNRLVGIANRN 406
Db 327 -----TITLENGLTENP--TLFTWINQGRFYTRNSRDILDVDFISFTGNQMA----- 373
Qy 407 RSTVATTGTIIIGERTG---PPTTKLIPESY---KSVITDROVTPSPFPPIYFT 459
Db 374 -FHTNDRNLIWGAHVGNISQDTSKVFPFYRNKPKIDKVEIVHRR-----YSD 422
Qy 460 INQIELYLNNSPNKLTYSAGNLSNDKKTDFQPVKQCKPIINPNCPLSPSYNSYSHIL 519
Db 423 IIVEMIFPNS-SEVPYSSNSTIENNYKRTDSYMPKQTK-----NKEYGHTL 471
Qy 520 SQFSLFNYSYKIGIALNLYTGALGTHSSVNRNNAISDKIITMIPA KGNSLDTNSKVI 579
Db 472 SYIKTDNYIFSV---VRERRVAFSWTHTSVDFQNTIDLDNITQIHAKALKVSSDSKIV 528
Qy 580 EGPCHTGNLYVLOSQRLEITCR--TPNSTQSYVIRLYATNGAGNTLPNISLTIPGVIG 638
Db 529 KGPCHTGGDLVILKDS--MDPRVFLKNVSRQVQVIRIYATNA-----PKTTVLTGIDT 581
Qy 639 IPPORLANTFSGTNYN--NLQYGDGYFQFPSTV-----TLPLNRNIPFIFNRADV 687
Db 582 ISVE-LPSTTSRQPNATDLTYADFGVYTFPRTPVNTKTFEGEDLLMT-----LYGTPNH 635
Qy 688 SNSILIIDKIEFIPITSSVRQNRKQKLETTQTQKINTFFTN 728
Db 636 SYNI-YIDKIEFIPITQSVDLYTEKQIEKTKIVNDLVFN 675

RESULT 7
Q8VNX2 BACTV
ID Q8VNX2 BACTV PRELIMINARY; PRT; 650 AA.
AC Q8VNX2
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry29Aa protease.
GN Name=cry29Aa;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=79672;
RN
RP NUCLEOTIDE SEQUENCE.
RA Delecluse A., Orduz S.;
RL Submitted (DDBJ/EMBL/GenBank/DBJ databases.
EMBL; AJ251977; CAC80985.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 650 AA; 74435 MW; D0CB846377CC517B CRC64;

Query Match 21.6%; Score 843; DB 2; Length 650;
Best Local Similarity 32.4%; Pred. No. 5.5e-45;
Matches 239; Conservative 126; Mismatches 276; Indels 96; Gaps 26;

Qy 1 MNQ-NNNVEIIDSKNLSYPSNRNIDHSRYPTNNPQNTNYKEWLNMC--QGNQY 57
Db 1 MNSFQNKNEYILNAP--SSISNIPNNYSKYPIANTLNQTMQNTYKDWNTMCAIDNNLK 58
```

QY	58	YGDNFETASADTIAAASACTIVSGTLGAGIGGLTISGPIGLIIGAIISFGTLITVFWP	117	RP	NUCLEOTIDE SEQUENCE.
Db	59	SINPFENLQNSVLGPAITAAIASLISAPITGTSIAGTAJAAI-----IPILWP	111	RC	STRAIN=402-72;
QY	118	AGEQDKTVVTFQIKMGEIFVDVTLTESIKQKQLQTLLEGFRQILQSNTALDDWRKLRLQ	177	RX	MEDLINE=88185334; PubMed=28333395;
Db	112	S--QENNLDPKLLAISATLYSQDQVRREDALTRLESKDSVKYPENAFTFIN-----	164	RA	Chungjatupornchai W., Hoefte H., Seurinck J., Angsuthanasombat C., Vaeck M.;
QY	178	APGLPSSALQQAALTKIRFENVHDFIREIFGQFLETYKTLPIIYAQAAPHNLQ	237	RA	"Common features of Bacillus thuringiensis toxins specific for Diptera and Lepidoptera.";
Db	165	-----NPNST---NTTVRRFQEVNGRFVSGMAFFRAKNYEPILLSTYAQAARLHLHLR	217	RT	Eur. J. Biochem. 173:9-16(1988).
QY	238	QGAELADEWNADHPISOIEBNAAGTSDDYKLLKENIPKYSNCANYREGNKLREPNM	297	RL	[3]
Db	218	DGITYAEKMLNSRGDDM-----PGDLLYKEFNKYCNEYIEHCIKWYNBSLSLKS-VGA	271	RN	NUCLEOTIDE SEQUENCE.
QY	298	RWSIFNDYRYMTITVLDITIAQSFYDIKRYKDSIGRIGIKTELAREIYTTTEINFDRLT	357	RA	Sen K., Honda G., Koyama N., Nishida M., Neki A., Sakai H., Himeno M., Komano T.;
Db	272	NWLEYNQYRTFLTASVLDVLSLFSYDPRLYKERLS-----VEILTRKLYTDPINYHRGI	326	RT	"Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis.";
QY	358	YLSIQPNLAMEYNLTRSGURLPSFLDELIFPYKNETYGNRLVGIANRNRSTVATTGTEI	417	RL	Agric. Biol. Chem. 52:873-878(1988).
Db	327	SLEADES-----KYLEPT---LFTQLYTLTFYS-NIFY--NYMGHTN---TYRYSPOK	372	RN	NUCLEOTIDE SEQUENCE.
QY	418	IYGERGPGPTTKTLIPESY--KVSIVTDQVTPSPFPNIVETINQIELYLNNSPSNKL	475	RX	MEDLINE=88329719; PubMed=2901387; DOI=10.1016/0378-1119(88)90229-6;
Db	373	IFAEBSFGKQS-----SYIDKVPVI-----PNDKSIYKIRAYDNHNGLFNV	414	RA	Angsuthanasombat C., Chungjatupornchai W., Kertbundit S., Luxanani P., Sattasatian C., Wilairat P., Panyim S.;
QY	476	TSAGGNLSNDKKTDFQFPVKDKCKPIINPNCPLPSVNSYSHLSOFSLFNYSYKIGLAL	535	RT	"Cloning and expression of 130-kd mosquito-larvicidal delta-endotoxin gene of Bacillus thuringiensis var. israelensis in Escherichia coli.";
Db	415	MYGFWGDEKQ---IQKIIGSGSTEIYKNC-----THRLADVISHDLDEK-----	458	RL	Mol. Gen. Genet. 208:384-389(1987).
QY	536	NILYTGAHSHSVNRNNAISDKITMIPAIGNSLDNTNSKVIPEGHTGMLVYLSQ	595	CC	-!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut epithelial cells of mosquitoes.
Db	459	NKCYSPA--WTSTISLENIKNDIITQIPAVKAYQLGVQSVIKGPGHTGGDLNLKSN	516	CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
QY	596	GRLEITCR-TPNSTQSYVIRLYATGAGNTLNPISITIPGVIGIPQR--LNNTFSGTV	652	CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
Db	517	DYURISQHLNSVTKYFVRIRATNGSLNTRPIIITIP---GMTPQGMVLONTFSGTG	573	CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
QY	653	YNNLQXGDFGYFPSPSTVTLPLNRNIPFPINRADV--SNSILIIDKIEFIPITSSVRQNR	711	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
Db	574	YSNLEQNFGYKEFLKEVTLNPNQISLTLNRSDQNSLILLDDRIEFLPITPSIRKSXE	633	DR	EMBL; X07082; CAA30114.1; -; Genomic DNA.
QY	712	KQKLETIQTKINTFFTN 728		DR	EMBL; X05692; CAA29174.1; -; Genomic DNA.
Db	634	QONLEKNQKTVNKLFFN 650		DR	EMBL; D00247; BAA00178.1; -; Genomic DNA.
				DR	EMBL; M20242; BAA22337.1; -; Genomic DNA.
				DR	EMBL; X07423; CAA30312.1; -; Genomic DNA.
				DR	PIR; S00398; USB981.
				DR	PDB; 1W99; X-ray; A=84-641.
				DR	InterPro; IPR001178; Endotoxin.
				DR	InterPro; IPR005638; endotoxin.C.
				DR	InterPro; IPR005639; endotoxin_N.
				DR	Pfam; PF03944; Endotoxin_C; 1.
				DR	Pfam; PF00555; Endotoxin_M; 1.
				DR	Pfam; PF03945; Endotoxin_N; 1.
				KW	3D-structure; Plasmid; Sporulation; Toxin.
				FT	CONFLICT 51 51 V -> D (in Ref. 4).
				FT	CONFLICT 65 65 T -> S (in Ref. 4).
				FT	CONFLICT 193 201 LINAQEWSL -> PHKCTRMVY (in Ref. 4).
				FT	CONFLICT 203 204 RS -> C (in Ref. 3).
				FT	CONFLICT 205 206 AG -> C (in Ref. 4).
				FT	CONFLICT 205 205 A -> R (in Ref. 1).
				FT	CONFLICT 272 272 Y -> L (in Ref. 3).
				FT	CONFLICT 325 325 D -> Y (in Ref. 3).
				FT	CONFLICT 364 401 FGSNLTHTQIQLNSNVYKISITDSSPSNRVTKMDFYKI -> LVQIYLIRKPNLILVILKLSQILAPPLIELQKWISTKF (in Ref. 4).
				FT	CONFLICT 467 467 K -> N (in Ref. 4).

RESULT 8

CR4BA_BACTI	STANDARD;	PRT; 1136 AA.
ID	CR4BA_BACTI	
AC	P05519; P11782; P16479;	
DT	01-NOV-1988 (Rel. 09, Created)	
DT	10-MAY-2000 (Rel. 39, Last sequence update)	
DT	13-SEP-2005 (Rel. 48, Last annotation update)	
DE	pesticidal crystal protein cry4Ba (insecticidal delta-endotoxin	
DE	CryIVB(a)) (crystalline entomocidal protoxin) (128 kDa crystal	
DE	protein).	
GN	Name=cry4Ba; Synonyms=bt8, cryD2, cryIVB(a), isrH3;	
OS	Bacillus thuringiensis subsp. israelensis.	
OG	Plasmid 72 Kb.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	
OC	Bacillus cereus group.	
OX	NCBI_TaxID=1430;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=88157738; PubMed=2831510;	
RA	Tungpradubkul S., Sattasatian C., Panyim S.;	
RT	"The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delta-endotoxin gene of Bacillus thuringiensis var. israelensis.";	
,RL	Nucleic Acids Res. 16:1637-1638(1988).	


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QY 704 SSVQRNREKOKJETIQTKINTEFTNHTNTLNTIEATNYDID 744
Db 635 QSVLDETENQLESEREVNALFTNDKALNIGTTDIDID 675

RESULT 10
Q8VNX1_BACTV
ID Q8VNX1_BACTV PRELIMINARY; PRT; 688 AA.
AC Q8VNX1;
DT 01-MAR-2002 (TremBrel. 20, Created)
DT 01-MAR-2002 (TremBrel. 20, Last sequence update)
DE Cry30Aa protein.
GN Name=cry30Aa;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=79672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Delecluse A., Orduz S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251978; CAC80986.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; F:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 688 AA; 77844 MW; 7E0D57085BD7B3A9 CRC64;

Query Match 20.58; Score 802; DB 2; Length 688;
Best Local Similarity 32.4%; Pred. No. 2.4e-42;
Matches 246; Conservative 109; Mismatches 274; Indels 130; Gaps 31;

QY 1 MNO-NNNNEYIID-SKNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKWLNMCCQNTQY 58
Db 1 MNSYENKNEYIILDTSQKNSMNR---YSKYPILTNNPKVPLQNTNYKWLNMCCQITPL 57
QY 59 GDNFETPASADTTAAVSAGTIVSGTLGAGTGTSGIPGIGTIGAIISFGTLITVFWPA 118
Db 58 CTPIDTDSKLVAATAIKVIGAI-----FKSMPPGPGAAVGLVLKSPSTIIPILWP- 105
QY 119 GEODKT-VMTQFIKMG-EIFVDTPLTESI-K-OLKLTLEGFRQILQSYNTALDDW 170
Db 106 --NDKTPIKWKEFTKQGLQFRPELGRDAIEIIGNDVQAEYNSLE---IMMRDPENKPAW 160
QY 171 RLKRLQAPGLPSSALQQAALTKIRFENVHNDFIREFPGFOL-ETYKTLILLPIYAQA 229
Db 161 E-----SNRTRNAIAVTAFTSVNTQILKRFELIAENRPAFLNLAQTA 208
QY 230 NFHLNLQQAELADEWADIHPSQIEPNAGTSDDYKLLKENIPKSYNCANTYREGN 289
Db 209 NIDLILYQGSVYGDKWADVADINNRSTSP--FSSKDYVQSLGKIKDYNTYCAETYSNLT 266
QY 290 KLRNEPNWRMSIENDRYVNTITVLTIAQFSFVDIKRYKDSIGRIGGIKTELTRIYTT 349
Db 267 ILNKKPHIQNDIYNRYRREAILGALDLVALFPNDICVPTQ-----TKTELTRKYMP 320
QY 350 EINFDRILTYLEI--QPNLAIMEYNLTRSGLRFLSFLDELIFYTKNETYG-----NRLVGI 402
Db 321 SF-----YLQAQQRDIEVENQLTHPP-SLTWLNELNLYTIRERFNPVLQVASLSGL 373
QY 403 ANNRSTY-ATTGTEIHYGE-RTGPPPTKTLIPFESYKVSIVTDQVTPTPSPPNFYFTI 460
Db 374 QATSRYTQNTTISNPVQGVREGTPTKISLANYYIKLFMSQYRPNDCPLPSG---I 429

RESULT 11
Q75VA2_BACTE
ID Q75VA2_BACTE PRELIMINARY; PRT; 683 AA.
AC Q75VA2;
DT 05-JUL-2004 (TremBrel. 27, Created)
DT 05-JUL-2004 (TremBrel. 27, Last sequence update)
DE Putative mosquitocidal toxin.
GN Name=cry30Aa like;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1436;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=INA288;
RA Ikeya T., Yamaya K., Ito T., Sahara K., Bando H., Asano S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB125059; BAD00052.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; F:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 683 AA; 77438 MW; 488B477B876BFDCA CRC64;

Query Match 20.4%; Score 796; DB 2; Length 683;
Best Local Similarity 31.4%; Pred. No. 5.8e-42;
Matches 245; Conservative 107; Mismatches 264; Indels 164; Gaps 32;

QY 8 EYEIDSKNLSYPSNRNIDHSRYPTNNPQNPLQNTNYKWLNMCCQNTQYDGNFETPAS 67
Db 9 EYEILDA--LPNYSNNWVAYSRYPLANNPQVPLQNTSYKWLNMCCQ-----TINP 56
QY 68 ADT-----IAAVSAGTIVSGTLGAGTGTSGIPGIGTIGAIISFGTLITVFWPAGEQD 122
Db 57 LCTPINIDISLAAASIAVVGSI-----LIPGGEALGVLTFTSTILPILNPNGE-- 108
QY 123 KTVWTFQIKMG-EIFVDTPLTESI-KQLKLTLEGFRQI---LQSYNTALDDWRKLRLOA 178
Db 109 TKIWTDFAEERGLQFRPELGRDAIEILVTGVKSGYNALKNRMENFEQAFTKKK----- 161
QY 179 PGLPSSALQQAALTKIR-FENVNDFIREFPGFOL-ETYKTLILLPIYAQAANFHLNLL 236
Db 162 -GNRTSRNAEQV-----IRDFDSVRDKVIDLKNYMINPENKPAFLNLYAQTALDILY 215
```

QY 237 OQGAELADENADHPQSIENAGTSDYYKLLKENIPKSYNYCANYTREGINKLRNEPN 296
Db 216 QRGAVYGDWEKINGS-ISPFG-SKDYVESLTKIEEYNYCAETVRSNLKKNKPN 273
QY 297 MRWISFENDYRYMTITVLDTTAQSFYDIKRYKDSIGRIGIKTELREIYTTTEINFDRL 356
Db 274 ISWTYKYRREALTGALDVALFPNDMLHP-----AATKTELFRKIYMPFSGLOQS 327
QY 357 TYLEIQPNLAIMEYNLTRSGRLFSFLDELIFYTKNETYG-----NRLVGIANRRTYA 411
Db 328 NYFQ---SLEGLENALTHPP-SLFTWLNELNLYTVRENFNPAQVSSLSGLQARSRYQN 383
QY 412 TTGTE-IYIGERTGPPTKILIPESYKSVITDQVTPSPFFNIYFTINQIBLY---L 467
Db 384 PTILDNPAQVGRNGTSTQIGLNNLFVYKLSMSQYHHPNDCSIAAG-----ISDMTFYKSDY 439
QY 468 NNSPSNKLTYSAGNLSNKKTTDFQFPVKDKCPIN-----NCLPSYNSYS-----H 517
Db 440 NGNASATQYQAGRTNN-----VINTFNGQKASSNNISIKQTKH 482
QY 518 ILSQFSL-----FNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITMI 564
Db 483 ILSDIKMIYPTGMYQVYDGYSF-----AWHTSVDPDNLIVPNRITQI 528
QY 565 PAIKGNSLDNTSKVIEGPGHTGGLNVLVYLSQGRLEICRTPNSTQSYIURLRYATNAGN 624
Db 529 PAVKALGISTDSKVVGPFVFTGDLKLLKLOATIRI--KTDHANTRYKIRVRYASN--AN 584
QY 625 T-----LPN-LSLTICGVIGIPQRLNNTFSGTNVNNLOVDFGYPFPSTVTLPLNRN 677
Db 585 TPVLSSQNLTAVTFP-----QTITHSTISELOQKDPQYVTFPG-----624
QY 678 IPFIENRADVNSNI-----LIIDKIEPIPTSSVRQNRKQKLETIQKINTPTFTN 728
Db 625 -EFIMDXPSIDVARGVQNDENDIWDRIEPLITQSVLDVTEBQNIKESQKAVNDLFIN 683

RESULT 12
CR8BA_BACUK
ID CR8BA_BACUK STANDARD; PRT; 1169 AA.
AC Q45705;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry8Ba (Insecticidal delta-endotoxin
DE CryVIIIa(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
DE protein)
GN Name=cry8Ba; Synonyms=50C(b), cryVIIIa(a);
OS Bacillus thuringiensis subsp. kumamotoensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=132267;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=NRRL B-18746 / PS50C;
RA Michaels T.E., Foncecerra L., Narva K.E.;
RT "Process for controlling scarab pests with Bacillus thuringiensis
RT isolates";
RL Patent number WO9315206, 05-AUG-1993.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects. Active on various scarabaeid beetles.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----; U04365; AAA21118.1; -, Genomic_DNA.
DR HSBP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1169 AA; 133544 MW; 22EEFCF5BD699909 CRC64;

Query Match 20.3%; Score 791.5; DB 1; Length 1169;
Best Local Similarity 28.0%; Pred. No. 2.3e-41;
Matches 217; Conservative 151; Mismatches 297; Indels 109; Gaps 28;

QY 1 MNQNNNEYEIIIDSKNLSYPSNRNIDHSRYPTNNPNQPLQNTNYKEMLANCOGN-TOYG 59
Db 1 MSPNNQNEYEIIIDATPSTSVN---DSNRYPFANEPTNALQNMDYKDYLLKMSAGNVSEYP 57

QY 60 DNFETASADTIAAVSAGTIVSGTLGAGIGLTSISQPIGIIIGAIISIFGTLITVFPAG 119
Db 58 GSPFVFLSEQD--AVKAAIDIVGKLLTGLG-----VPFVGPVLSLYTQIDILWPS- 106

QY 120 EQKTVVWQIKGEIIPVDPPLTESIKQLKQTLLEGPRQILQSYNTALDDWRKUKRLQAP 179
Db 107 -KQKQWEIPEQVEELINQIAEYARNKALSELGLGNNYQLYLTALKEWKE----- 158

QY 180 GLPSSALQAAALTLKRFENVHDFIREIPGQLEYKTLILLPIYAAANFHLNLAQOG 239
Db 159 --NPNGS--RALRDVRNRFELDSLFTQYMPSPRVNTFVFPFLTVYVYTAANLHLLURDA 214

QY 240 AELADENADHPQSIEPNAGTSDYYKLLKENIPKSYNYCANYTREGINKLRNEPNRW 299
Db 215 SIFGEWGL-----STSTNNYNRQMKLTAEYSDHCVKWEYGLAKLKSSAKQW 265

QY 300 SIFNDVRYMTITVLDTTAQSFYDIKRYKDSIGRIGIKTELREIYTTTEINFDRLTYL 359
Db 266 IDYNQFERREMTLVLDVVALFSNYDTRTYPLA-----TTAQLTREYVT-----DPLGAV 314

QY 360 EIOPNL-----AIMEYNLTRSGLR---LFSFLDELIFYTKNETY--GNRLVGIANRRT 409
Db 315 DV-PNIGSWYDKAPSFSEIEKAAIRPHVFDYITGLTVYTKGRSFTSDRYMYRWAGHQIS 373

QY 410 YATTGTEIIGERTGPPTKTL-----IPESYKV-SIVTDQVTPSPFPNI----- 456
Db 374 YKHIGTSSTETQMGV--TNQNLQSTNFDFTNYDIYKLSNGAVLLDIVPGYTYTFPGM 431

QY 457 -----YFTINQIEIYLNNSPNKLTYS--AGNLSNDKKTDPQFPVKDKCKPIINPCLPS 511
Db 432 PETEFFMVNQL-----NNTRKTLTYKPASKDIIIDRTDSELELPPEPESGQ-----PN 478

QY 512 YNSVSHLSQFSLFNYSYKIGLALNLYTGALGTHSSVNRNNAISDKIITMIPAIGNS 571
Db 479 YESYSHRLGHIT-FIYS-----SSTSTYVPVFWSTHRSADLTNTVKSGETIQTIPGKSST 532

QY 572 LDYNSKVIIEGPGHTGGLNVLVYLSQ--GRLEITCTPNSQSYIRLRYATNAGNTLENIS 630
Db 533 IGRNTYIIKRGYTGGLDVALTDRIKSCFQMFIPES-QRFRIRIRVSNETS-----Y 585

QY 631 LTIPIGVIGIPQRLNNTFSGTNVNNLOVDFGYPFPSTVTLPLNRNIPFIENRADVNS 690
Db 586 ISLYGLNQSGTLKFPNQTSYKNKENDLTNDFKYIEYPRVISVNASNIQRLSIGIQTNTN 645

QY 691 ILIIDKIEPIPTSSVRQNRKQKLETIQKINTPTFTNHTKNTLNIEATNYDID 744
Db 646 LFILDRIEFIPVDTEAEATD---LEAAKKAVALFTN-TKDLQPGQVGTDEVN 695

RESULT 13
Q5W7N9_BACTU
ID Q5W7N9_BACTU PRELIMINARY; PRT; 688 AA.
AC Q5W7N9;


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Db 416 TS-----DVQINSISSNLABALSTL-----PGVTRAQFHYGSG-----IISVYG----- 456
Qy 488 KTTDFQFPVKDC-----KPIINPCLPSYNSHILSOFSLFNYSYK-----IGLAL 535
Db 457 -----QNNVLPOCHQNYNSIEELPNQSDPEPTVRSYSHRLSHITSFNSVOLNPNVLSGN 511
Qy 536 NILTGALGTHSVNRNNAISDKIITMIPAIGNSLDTSNKVIEGPGHTGCGNLVYLQSQ 595
Db 512 MPVVV-----WTHRSVDLNTTISDRITQLPVAVKASTLGAGAIVVKGPGFTGCDVIRRTSV 567
Qy 596 G-----BLEICTRPNSTQSYVIRLVATNGAGNTLPNISLTIPGVIGIPPORLNNFTSG 650
Db 568 GDFGTIRVSV-----TGSLTQQRIRFRYA-----STIDPFFVIRG-----G 605
Qy 651 TNYNNLQY-----GDFGYFOPPSTVTLPLNRNIPPIFNRA-DV-----SNSILII 694
Db 606 TTINFRTHMTSSGEESRYESYRTVEP-----STPFNTQSDIIRTSIQGLSGNGEYVL 661
Qy 695 DKIEFIPITSSVRQNRQKLETTQTNTKNTFTVHTKNTLMEATNVDID 744
Db 662 DRIEIPVNPPT---REABEDLEDAKAVAGLFT-RTRDGLQVNVTDYQVD 707

RESULT 15
CR3BA_BACTO
ID CR3BA_BACTO STANDARD; PRT; 659 AA.
AC P17969;
AD 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry3Ba (insecticidal delta-endotoxin
DE CryIIIB(a)) (Crystalline entomocidal protoxin) (75 kDa crystal
DE protein).
GN Name=cry3Ba; Synonyms=cryIIb, cryIIIB(a);
OS Bacillus thuringiensis subsp. tolworthi;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1442;
RN [1]
RC NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP STRAIN=43F;
RX MEDLINE=90206811; PubMed=2320431;
RA Sick A., Gaertner F.H., Wong A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi.";
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X17123; CAA34983.1; -; Genomic DNA.
CC EMBL; A07234; CAA00645.1; -; Unassigned DNA.
CC PIR; S10228; S10228.
CC HSSP; Q06117; 1J16.
CC SMR; F17969; 72-659.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; Endotoxin C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
KW

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SQ SEQUENCE 659 AA; 75159 MW; 5A5B214FF84168CA CRC64;
Query Match 18.2%; Score 710; DB 1; Length 659;
Best Local Similarity 28.9%; Pred. No. 1.6e-36;
Matches 217; Conservative 115; Mismatches 270; Indels 148; Gaps 31;
Qy 1 MNQNNNEVEIID-SKNLSYSPNRNDHSRYPYNNENQPLONTNYKEWLNMCQNTQYG 59
Db 9 MNPNNRSEYDTIKVTPNSELPFN-----HNQYPLADNPNSTLBELNYKEFLRMTADNST-- 62
Qy 60 DNFETPASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIAGIIISFGTLITVFPAG 119
Db 63 ----EVLDSSTVKDVGTSIVSQILGVG-----VFFAGALTSTFYQSFNAIWP-- 110
Qy 120 EQDKTVMTQFKMGEIPVDTPELTSIKQLKQLTLEGFRQILQSYNTALDDWRKLRLQAP 179
Db 111 --DADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQNNFEDYVNALDSWK----- 161
Qy 180 GLPSSALQQAALTLKIRPENVINDFIREIPGQLEYTKTLLPIYAAAFHNLILQOG 239
Db 162 -APVNLRSRSQDRIRELFQSAESHFERNMSPFAVSKFEVLFLPTAAANTHLLLLKDA 220
Qy 240 AELADEWNADIHPSQIEPNAGTSD--YYKLLKENIPKYSNYCANTYREGLNKLRNEP 296
Db 221 QVFGEEMGY-----SSEDIAEYFQRLKLTQQTIDHCVNNYVGLNSLRSTY 268
Qy 297 MRWSIFNDYRRYMTITVLDLIAQFSFYDIKRYKDSIGRIGIKTELTRREIYTTINFDR 356
Db 269 DAWKFNFRREMTLVLDLIVLFPFYDVRLYSK-----GVKTELTRDITFDPI-FTLN 321
Qy 357 TYLEIQNLAIMENLRSGLRFLPSFLDELIFTK-----NETVGNRLVGLIAR 405
Db 322 ALQEGYGTFFSIIENSRKP--HLFDYLRGIEFTLRPLPGYSGKDSFNWGSNY---VETR 376
Qy 406 NRSYATGTTEIIVGERTGPTTKTLIPPEYSKYIVTDQV--TPTSPPN--IYFTIN 461
Db 377 PSIGSNDTIISPPYGDKSIPIQK--LSFDGQKV-----RTIANDIAAFPDGKIYFGVT 430
Qy 462 QIELYLNNSPSNKL---TYSA-----GGNLSNDK---KTTDFQFPVKDCRPIINPNC 508
Db 431 KVDPSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPETTD--EPEK----- 478
Qy 509 LPSVNSYSHILSOFSLFNYSYKIGLALNIIYTGALGTHSVNRNNAISDKIITMIPA 568
Db 479 -----AYSHQLNVAECFLMDRRGTI--PEFT-----WTHRSVDPFNTIDAETITQLP 527
Qy 569 GNSLDTMSKVIIEGPGHTGCGNLVYLQ-----SQRLEITCRTPNSTQSYVIRLVATNGAG 624
Db 528 AYALSSGASIIIEGPGFTGCGNLFLKSSNSIAKPKVTLSAALLQRYRVRIRYAST---- 583
Qy 625 TLPNISLTIPGVIGIPPORLNNFTSGTNYNNLQY--GDFGY--FQFPSTVTLPLNRNIP 680
Db 584 --TNLRLFV-----QNSNDELVIYINKWNIDGLTYQTDFATS-----NSNMGF 628
Qy 681 IFNRAD-----VNSIILIIIDKIEPIPI 702
Db 629 SGTNDNFIIGAESFVSNEKIYIDKIEPIV 658

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Search completed: December 15, 2005, 10:54:56
Job time : 235 secs

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